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I, LEANNE MYNOTT, TEAM LEADER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. PO 6329 for a patent by THE NATIONAL UNIVERSITY OF SINGAPORE filed on 21 April 1997.

WITNESS my hand this
Twenty-ninth day of November 1999

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PROVISIONAL SPECIFICATION

for the invention entitled:

"Diagnosis of Parasites"

The invention is described in the following statement:

DIAGNOSIS OF PARASITES

The present invention relates generally to novel genetic sequences isolated from a parasitic protozoa which infects humans and other animals and the uses of said sequences as diagnostic agents for the detection of said protozoa in a biological sample. In particular, the present invention provides genetic sequences of the extrachromosomal genetic element of the malaria agents *Plasmodium berghei*, *Plasmodium vivax* and *Plasmodium malariae* and synthetic oligonucleotide derivatives, homologues, analogues and fragments thereof. The genetic sequences of the present invention are particularly useful in the diagnosis, prophylactic treatment and therapeutic treatment of humans and other animals which are capable of being infected by or are actually infected by protozoa such as *Plasmodium ssp.*, for example *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*, *P. gonderi*, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*, *P. reichenowi*, *P. rodhaini*, *P. schwetzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum*, *P. yoelii*, or *P. berghei*, amongst others. The invention provides further, a novel, reliable diagnostic assay for the detection of *Plasmodium ssp.* in humans and animals.

Bibliographic details of the publications referred to by author in this specification are collected at the end of the description. Sequence identity numbers (SEQ ID Nos.) for the nucleotide and amino acid sequences referred to in the specification are defined after the bibliography.

Throughout the specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers, but not the exclusion of any other element or integer or group of elements or integers.

More than fifty different species of *Plasmodium* can cause malaria in humans, monkeys, birds, fish, cattle and rodents. The development of diagnostic assays for the detection of *Plasmodium* in humans and animals is therefore highly desirable.

Human malaria, which is caused by *Plasmodium ssp.*, in particular *P. falciparum*, *P. vivax*, *P. malariae*, and *P. ovale*, remains one of the major health problems around the world.

Plasmodium vivax induces a moderate form of malaria, vivax malaria, characterized by periodic chills and fever, an enlarged spleen, anaemia, severe abdominal pain and headaches, and extreme lethargy. If left untreated, the disease tends to be self-limiting within a period of 10 to 30 days, but will recur periodically. Although the fatality rate of vivax malaria is low, the disease is highly debilitating and makes the patient more vulnerable to other diseases.

The incubation period ranges from 10 days to 4 weeks. Generally, paroxysms of chills and fever appear on the 14th day after the bite of an infected female anopheles mosquito. During this time the parasite has been multiplying in the liver cells of the patient. Paroxysms continue to recur every other day, as the parasite completes its 48-hour cycle of development, now in the blood. During the paroxysm, the patient first goes through a "cold stage" during which he has chilly sensations, his skin is blue, his teeth chatter and there is violent shaking. After an hour, the "hot stage" is ushered in, with a rise in temperature to as high as 107°F (41.7°C); the skin is hot and dry and the patient complains of severe headache. The fever lasts about 2 hours, and is followed by the "sweating stage", during which there is profuse perspiration, the temperature falls to normal, the headache disappears, and although weak and drowsy, the patient feels well.

Plasmodium ovale produces a disease very similar to vivax malaria.

Plasmodium malariae, the causative agent of quartan malaria, has an incubation period of 18-40 days. The paroxysms occur every 72 hours, and are longer and somewhat more severe than those accompanying vivax malaria.

Plasmodium falciparum-induced malaria (falciparum malaria) presents oedema of the brain and lungs and blockage of the kidneys, in addition to the symptoms associated with vivax malaria. Unless treated promptly, the fatality rate of falciparum malaria is high, especially in juveniles.

Paroxysms associated with falciparum malaria occur irregularly after a 12-day incubation period. They are severe, and accompanied by high temperatures. The so-called cerebral algid, haemorrhagic and pernicious types of malaria represent forms of falciparum malaria with different localizations of the parasite. In the cerebral type, the onset is delirium and coma, and death may occur in several hours without return to consciousness. "Black-water fever" or haemorrhagic malaria is a type in which haemolysis or dissolution of the red cells occurs, and dark urine due to the presence of haemoglobin is an outstanding feature. In the algid form, there are vomiting, diarrhea, and subnormal temperature.

The life cycle of the parasite and its course in the human body proceeds in the following way. The saliva of the mosquito contains the *Plasmodium* at the lance-shaped sporozoite stage of its life cycle. Upon inoculation of the host by biting, the sporozoites quickly migrate to the liver where they divide and develop into multi nucleated schizonts. Within 6 to 12 days, the schizonts disrupt and release into the blood the form known as *merozoites*. Each liver cell infected by one sporozoite releases into the blood stream from 10,000 to 30,000 merozoites. These later invade the host's erythrocytes where they grow and form more schizonts which, in turn, again divide, releasing more merozoites into the blood stream to repeat the cycle. The principal symptoms of malaria are associated with the rupture of the schizonts, the periodic lysis of the blood cells with release of merozoites and toxic wastes which cause the regular fevers and chills of malaria.

Neither vector control measures nor immuno or chemoprophylaxis have proven effective in eradicating the disease. Thus, more than ever, chemotherapy appears to be crucial in dealing with both the prevention and treatment of malaria. However, presently used drugs are constantly losing their efficacy due to the development of drug resistance by the parasite.

For example, drug resistance of *Plasmodium falciparum* to chloroquine has occurred in Bangladesh, Brazil, Burma, Colombia, Ecuador, Guyana (French), Guyana, India, Indonesia, Kampuchea, Malaysia, Nepal, Pakistan, Panama, Philippines, Surinam, Thailand, Venezuela, and Vietnam, amongst others. Therefore, the design of novel drugs is urgent.

Targets for drug design are generally nuclear-encoded gene products. However, inter-specific and developmental variation in nuclear gene expression has reduced the general efficacy of drugs which target such nuclear-encoded gene products.

Diagnosis of malaria is generally made by microscopic examination of blood films taken during episodes of fever, when the parasites may be seen. In general, the *Plasmodium* parasite is detected microscopically by examining finger prick blood samples for the presence of the morphologically distinct parasite using Giemsa stain solution (Shute *et al.*, 1980). This needs to be done by an experienced microscopist since *Plasmodium falciparum* and *Plasmodium vivax* are morphologically similar, albeit not identical. In view of the distinct epidemiologies of *P. falciparum* compared to *P. vivax*, it is important that diagnosis of infection by these species have a low error rate. Any incorrect diagnosis of falciparum malaria, for example, may be fatal for the patient. The microscopic technique is limited in so far as the method is slow and specialised personnel is required to perform the technique.

A variation of the standard microscopic assay, the quantitative buffy coat (QBC) technique is based upon the ability of parasite nucleoproteins to absorb acridine orange and fluoresce (Wardlaw *et al,* 1983). The fluorescent nucleoproteins are readily visible against a background of non-fluorescent red blood cells. Although the method is more sensitive than the standard microscopic assay, it suffers from the disadvantages associated with the standard microscopic assay. Furthermore, the requirement of costly fluorescence microscopes and centrifuges to perform the QBC assay, renders the method unrealistic in resource-limited settings which often lack even electricity.

Immunological tests, for example the ParaSight™ F test (Becton Dickinson) and the similar ICT Malaria P.f. test (ICT Diagnostics) detect the *Plasmodium falciparum* histidine-rich protein HRP2 in blood samples derived from patients. A major drawback associated with such methods is that they require *Plasmodium falciparum* gene expression to occur before the organism can be detected. Furthermore, as considerable variation in gene expression can occur between *Plasmodium ssp.*, these tests tend to be species-specific. For example, the ParaSight™ F test (Becton Dickinson) and ICT Malaria P.f. test (ICT Diagnostics) are specific for *Plasmodium falciparum* only and incapable of detecting other species. Furthermore, these tests, in particular the ParaSight™ F test (Becton Dickinson), are subject to a high proportion of false-negative detections, such that a higher than acceptable frequency of patients infected with a *Plasmodium ssp.* go undetected.

Immunological techniques such as the enzyme-linked immunosorbent assay (ELISA) or the radio immunoassay (RIA) which detect genus- and species-specific parasite antigens also exist. However, such methods are constrained by immunological cross-reaction between parasite and host antigens on the one hand and between parasite antigens and antigens derived from other microorganisms on the other hand. As a consequence, the susceptibility of immunological methods to false positive detection of *Plasmodium* is high. As already mentioned above, species-specific detection methods lead to a large number of false-negative detections.

Furthermore, as different *Plasmodium* antigens are expressed at different developmental stages, immunological techniques may only detect the parasite at certain stages of development. Such antigenic diversity displayed by *Plasmodium* is a major obstacle to the application of immunological techniques. In addition, radioisotope-based assays such as the RIA are impractical for field use. Immunological methods cannot distinguish between past and present infections.

State-of-the art diagnostic assays, which rely on the detection of *Plasmodium* genomic DNA in a sample, are species-specific and not capable of general application for any

Plasmodium ssp., in part because there is considerable variation in genomic DNA between *Plasmodium* species, such variation precluding the simultaneous detection of several *Plasmodium ssp.* in a single biological sample or alternatively, the use of a single DNA-based assay for the detection of any *Plasmodium ssp.* in a biological sample derived from a human or animal subject suspected of carrying the parasite.

As a consequence of the foregoing, there is a high demand for a reliable and simple technology for the diagnosis of *Plasmodium* in human and animal tissues.

Plasmodium ssp. possess additional genomes with potentially crucial functions (Wilson *et al.*, 1991). Until the present invention, very little was known about this extrachromosomal material. Furthermore, the function of the extrachromosomal plasmid-like element in the protozoans remains to be determined. To date, there is no clear evidence for DNA replication or functionally active gene products from the plasmid-like element.

In work leading up to the present invention, the inventors have discovered that the molecular composition, physical arrangement and nucleotide sequence of the extrachromosomal plasmid-like element is highly conserved in different *Plasmodium ssp.*

The inventors have utilised the high degree of homology between different *Plasmodium ssp.* in the design of reliable, genera-specific or species-specific diagnostic assays for the detection of *Plasmodium.* The diagnostic assays described herein provide a significant advantage over currently employed assays based upon the detection of *Plasmodium* genomic DNA.

Furthermore, the inventors have discovered that the assays described herein provide the added advantage of excluding the high frequency of false negative detection of *Plasmodium* in a biological sample to a greater degree than known diagnostics.

The inventors further contemplate the use of polypeptides encoded by the extrachromosomal plasmid-like element, and their homologues, analogues and derivatives, as targets for drug design and in the development of anti-malarial vaccines.

Accordingly, one aspect of the invention provides a diagnostic assay for the detection of *Plasmodium* in a biological sample derived from a human or animal subject, said assay comprising the detection of a *Plasmodium* extrachromosomal genetic element or a homologue, analogue or derivative thereof in said sample.

In an alternative embodiment, the invention provides a diagnostic assay for the detection of *Plasmodium* in a biological sample derived from a human or animal subject, said assay comprising the steps of hybridising a *Plasmodium ssp.* extrachromosomal genetic element probe or a homologue, analogue or derivative thereof to said sample and then detecting said hybridisation using a detection means.

According to this aspect, the *Plasmodium* detected using the invention may be any species of *Plasmodium* which carries an extrachromosomal genetic element.

In a preferred embodiment, the *Plasmodium* being detected is selected from the list comprising *P. falciparum*, *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*, *P. gonderi*, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*, *P. reichenowi*, *P. rodhaini*, *P. schwetzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum*, *P. yoelii,* or *P. berghei*, amongst others.

In a more particularly preferred embodiment however, the present invention is useful for the detection of a *Plasmodium* in biological samples derived from humans and the *Plasmodium* in such cases is selected from the list comprising *P. falciparum*, *P. vivax*, *P. malariae* and *P. ovale*, amongst others.

The term "biological sample" as used herein shall be taken to refer to any organ, tissue, cell, exudate, nucleic acid, protein, nucleoprotein or other material which is derived from a living or once-living organism. Accordingly, a biological sample may be prepared in a suitable solution, for example an extraction buffer or suspension buffer. The present invention extends to the diagnosis of biological solutions thus prepared, the only requirement being that said solution at least comprises a biological sample as described herein.

The biological sample to be tested according to the invention, is derived from a human or animal species, in particular a human or animal which is capable of being infected by a *Plasmodium*. A particular advantage of the present invention is that it may be readily adapted to facilitate the analysis of any biological sample derived from a human or other animal. Those skilled in the relevant art will know how to modify the assay of the invention for the purposes of adapting said assay to the analysis of different biological tissues, where relevant or indicated, without any undue experimentation.

In a particularly preferred embodiment, the biological sample may be derived from the blood tissue of a human or animal subject, or cells, nucleic acid molecules and exudates derived therefrom, for example buffy coat, plasma, DNA or RNA, amongst others. The use of dried blood spots derived from human subjects as biological samples for the performance of the assays described herein is particularly contemplated by the invention.

The term "extrachromosomal genetic element" shall be taken to refer to any nucleic acid molecule, in particular DNA or RNA, which comprises a part of the complete genetic material of a *Plasmodium ssp.* but which does not comprise a part of a *Plasmodium ssp.* chromosome or a direct gene product thereof. An extrachromosomal genetic element of a *Plasmodium ssp.* may or may not replicate independently of the *Plasmodium* genome, such that the copy number of said genetic element may vary between *Plasmodium* cells.

Accordingly, a *Plasmodium* extrachromosomal genetic element as hereinbefore defined may be a linear or circular DNA molecule. In this regard, a linear DNA molecule may

resemble, at the nucleotide sequence level at least, mitochondrial DNA (Suplick *et al*, 1988), while a circular DNA molecule in a *Plasmodium* may be a plasmid or plasmid-like molecule which may resemble a vestigial plastid genome (Gardner *et al*, 1991; Howe *et al*, 1992).

In a preferred embodiment of the invention, the *Plasmodium* extrachromosomal genetic element is a plasmid or plasmid-like DNA molecule comprising approximately 30-35kb of nucleotides in length.

Furthermore, the diagnostic assay of the present invention is useful for the detection of a *Plasmodium* extrachromosomal genetic element or a *Plasmodium*-derived extrachromosomal genetic element, regardless of whether or not said genetic element expresses or is capable of expressing a polypeptide product.

The term "*Plasmodium*-derived" as used herein shall be taken to refer to an integer which, although it originates from a *Plasmodium ssp.* is not necessarily present in its natural state. For example, an extrachromosomal genetic element may be derived from a *Plasmodium ssp.* if it has been purified or partially purified and/or modified by digestion with restriction endonucleases or other DNA-modifying enzymes, to produce an analogue or derivative molecule.

The *Plasmodium* extrachromosomal genetic element probe may be a plasmid or plasmid-like molecule derived from a *Plasmodium ssp.* which is capable of infecting a human or animal subject.

Wherein the probe is a plasmid or plasmid-like extrachromosomal genetic element or a homologue, analogue or derivative thereof, it is preferred that it is derived from a species of *Plasmodium* other than *P. falciparum*.

In a particularly preferred embodiment, the plasmid or plasmid-like extrachromosomal genetic element probe or a homologue, analogue or derivative thereof, is derived from

Plasmodium berghei, *Plasmodium vivax*, or *Plasmodium malariae*.

However, in a more particularly preferred embodiment of the invention, the plasmid or plasmid-like extrachromosomal genetic element probe is at least 95% identical to one or more of the sequences set forth in SEQ ID NOs:1-10 or a complementary nucleotide sequence, or a homologue, analogue or derivative thereof.

Alternatively, the plasmid or plasmid-like extrachromosomal genetic element probe is capable of hybridising under high stringency conditions to one or more of the sequences set forth in SEQ ID NOs:1-10 or to the *Plasmodium vivax* or *Plasmodium malariae* sequences set forth in Figure 9, or a complementary nucleotide sequence or a homologue, analogue or derivative thereof.

In a further alternative embodiment, the *Plasmodium ssp.* extrachromosomal genetic element probe preferably comprises a sequence of nucleotides of at least 15 nucleotides, more preferably at least 25 nucleotides, even more preferably at least 50 nucleotides and even more preferably at least 100 nucleotides or 500 nucleotides derived from the sequence set forth in SEQ ID NOs:1-4 or to the *Plasmodium vivax* or *Plasmodium malariae* sequences set forth in Figure 9, or a complement or a homologue, analogue or derivative thereof.

In a most particularly preferred embodiment, the plasmid or plasmid-like extrachromosomal genetic element probe comprises a nucleotide sequence set forth in any one or more of SEQ ID NOs:1-10 or the *Plasmodium vivax* or *Plasmodium malariae* sequences set forth in Figure 9, or a complementary nucleotide sequence, or a homologue, analogue or derivative thereof.

For the purposes of nomenclature, the nucleotide sequences set forth in SEQ ID NOs:1-4 correspond to one strand of the PSI-PL470, PLH-PPH, PRB and PWQ genes, respectively, of the 30.7kb *plasmodium berghei* plasmid-like extrachromosomal genetic element. The inventors have shown that the extrachromosomal genetic element is

transcriptionally-active, using reverse transcription polymerase chain reaction (RT-PCR), and encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA polymerase subunits, amongst others.

The nucleotide sequences set forth in SEQ ID Nos:5-10 correspond to synthetic oligonucleotide sequences derived from the *Plasmodium* extrachromosomal genetic element of *P. berghei*.

The nucleotide sequence Pm1/S in figure 9 relates to the extrachromosomal genetic element of a *P.malariae* isolate.

The nucleotide sequences designated Pv12/P, Pb13/P, Pv15/I, Pv16/L, Pv17/S in Figure 9 relate to extrachromosomal genetic element sequences of different *P.vivax* isolates.

For the present purpose, "homologues" of a nucleotide sequence shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as the nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence within said sequence, of one or more nucleotide substitutions, insertions, deletions, or rearrangements.

"Analogues" of a nucleotide sequence set forth herein shall be taken to refer to an isolated nucleic acid molecule which is substantially the same as a nucleic acid molecule of the present invention or its complementary nucleotide sequence, notwithstanding the occurrence of any non-nucleotide constituents not normally present in said isolated nucleic acid molecule, for example carbohydrates, radiochemicals including radio nucleotides, reporter molecules such as, but not limited to biotin DIG, alkaline phosphatase or horseradish peroxidase, amongst others.

"Derivatives" of a nucleotide sequence set forth herein shall be taken to refer to any isolated nucleic acid molecule which contains significant sequence similarity to said sequence

or a part thereof. Generally, the nucleotide sequence of the present invention may be subjected to mutagenesis to produce single or multiple nucleotide substitutions, deletions and/or insertions. Nucleotide insertional derivatives of the nucleotide sequence of the present invention include 5′ and 3′ terminal fusions as well as intra-sequence insertions of single or multiple nucleotides or nucleotide analogues. Insertional nucleotide sequence variants are those in which one or more nucleotides or nucleotide analogues are introduced into a predetermined site in the nucleotide sequence of said sequence, although random insertion is also possible with suitable screening of the resulting product being performed. Deletional variants are characterised by the removal of one or more nucleotides from the nucleotide sequence. Substitutional nucleotide variants are those in which at least one nucleotide in the sequence has been removed and a different nucleotide or nucleotide analogue inserted in its place.

The present invention encompasses all such homologues, analogues or derivatives of a *Plasmodium* extrachromosomal genetic element, subject to the proviso that said homologues, analogues or derivatives are useful in the performance of at least one assay format as described herein.

The inventors have discovered that the extrachromosomal genetic element of *Plasmodium* is particularly useful as a marker of *Plasmodium* infection in a human or animal subject, because the detection of said element is not subject to the disadvantages of other assay methods, in particular the prevalence of false negative detection. As a consequence, fewer numbers of *Plasmodium*-infected hosts escape detection, by screening such hosts for the presence of the extrachromosomal genetic element according to the embodiments described herein (1% or less false negative detection compared to 3% or more for other methods), than by screening for the presence of other *Plasmodium*-expressed genes or by screening for the expression products of said genes.

Furthermore, the present invention is a procedure for assaying or identifying *Plasmodium* in a biological sample, in particular a biological sample which comprises a dried

blood spot.

The present invention clearly contemplates diagnostic assays which are capable of both genera-specific or species-specific detection. Accordingly, in one embodiment, the *Plasmodium ssp.* extrachromosomal genetic element probe or homologue, analogue or derivative thereof comprises DNA capable of being used to detect multiple *Plasmodium ssp.* In an alternative embodiment, the *Plasmodium ssp.* extrachromosomal genetic element probe or homologue, analogue or derivative thereof comprises DNA capable of being used to detect a particular *Plasmodium ssp.*

The inventors have discovered further that the coding region of a *Plasmodium* extrachromosomal genetic element is highly-conserved in different *Plasmodium ssp.*, while there is much more variation at the nucleotide level in the non-coding regions. Whilst not being bound be any theory or mode of action, the more highly conserved sequences in the extrachromosomal genetic element derived from a particular species of *Plasmodium* are particularly useful as genera-specific probes for the detection of any *Plasmodium*, while the less-conserved sequences of said element may be useful as species-specific probes for the detection of a sub-group of *Plasmodium*, for example a sub-group which infects humans or primates as opposed to other animals, or which induces a specific form of malaria in humans.

Furthermore, the diagnostic assay of the present invention may also be adapted to a genera-specific or species-specific assay by varying the stringency of the hybridisation step. Accordingly, a low or lower stringency hybridisation may be used to detect several different species of *Plasmodium* in one or more biological samples being assayed, while a high or higher stringency of hybridisation is used to detect the presence of a specific species of *Plasmodium*.

For the purposes of defining the level of stringency, a low stringency is defined herein as being a hybridisation and/or a wash carried out in 6xSSC buffer, 0.1% (w/v) SDS at 28°C. A moderate stringency is defined herein as being a hybridisation and/or wash carried out in

2xSSC buffer, 0.1% (w/v) SDS at a temperature in the range 45°C to 65°C. A high stringency is defined herein as being a hybridisation and/or wash carried out in 0.1xSSC buffer, 0.1% (w/v) SDS at a temperature of at least 65°C. Those skilled in the art will be aware of equivalent reaction conditions to those described herein for defining the hybridisation stringency.

Generally, the stringency is increased by reducing the concentration of SSC buffer, and/or increasing the concentration of SDS and/or increasing the temperature of the hybridisation and/or wash. Those skilled in the art will be aware that the conditions for hybridisation and/or wash may vary depending upon the nature of the hybridisation membrane or the type of hybridisation probe used. Conditions for hybridisations and washes are well understood by one normally skilled in the art. For the purposes of clarification of the parameters affecting hybridisation between nucleic acid molecules, reference is found in pages 2.10.8 to 2.10.16. of Ausubel *et al.* (1987), which is herein incorporated by reference.

The detection means according to this aspect of the invention may be any nucleic acid-based detection means, for example nucleic acid hybridisation techniques or polymerase chain reaction (PCR). The invention further encompasses the use of different assay formats of said nucleic acid-based detection means, including restriction fragment length polymorphism (RFLP), amplified fragment length polymorhism (AFLP), single-strand chain polymorphism (SSCP), amplification and mismatch detection (AMD), interspersed repetitive sequence polymerase chain reaction (IRS-PCR), inverse polymerase chain reaction (iPCR) and reverse transcription polymerase chain reaction (RT-PCR), amongst others.

Wherein the detection means is a nucleic acid hybridisation technique, the *Plasmodium* extrachromosomal genetic element probe may be labeled with a reporter molecule capable of producing an identifiable signal (e.g. a radioisotope such as ^{32}P or ^{35}S or a biotinylated molecule). According to this embodiment, those skilled in the art will be aware that the detection of said reporter molecule provides for identification of the *Plasmodium* extrachromosomal genetic element probe and that, following the hybridisation reaction, the

detection of the corresponding *Plasmodium ssp.* extrachromosomal genetic element in the biological sample is facilitated.

Wherein the detection means is an RFLP, nucleic acid derived from the biological sample, in particular DNA, is digested with one or more restriction endonuclease enzymes and the digested DNA is subjected to electrophoresis, transferred to a solid support such as, for example, a nylon or nitrocellulose membrane, and hybridised to the *Plasmodium* extrachromosomal genetic element probe as hereinbefore defined, optionally labeled with a reporter molecule. According to this embodiment, a specific pattern of DNA fragments is hybridised to the *Plasmodium* extrachromosomal genetic element probe, said pattern optionally specific for a particular *Plasmodium ssp.*, to enable the user to distinguish between different species of the parasite.

Wherein the detection means is a polymerase chain reaction or a variant of same, one or more nucleic acid primer molecules of at least 15 contiguous nucleotides in length derivable from the *Plasmodium* extrachromosomal genetic element probe as hereinbefore defined, or its complementary nucleotide sequence or a homologue, analogue or derivative thereof, is hybridised to the biological sample comprising nucleic acid or alternatively, to nucleic acid derived from said sample and nucleic acid copies of the *Plasmodium* extrachromosomal genetic element present in said sample or a part or fragment thereof are enzymically-amplified.

Those skilled in the art will be aware that there must be a sufficiently high percentage nucleotide sequence identity between the *Plasmodium* extrachromosomal genetic element probe(s) and the sequences in the template molecule to which it(they) hybridise. As stated previously, the hybridisation conditions may be varied to promote hybridisation.

Preferably, the *Plasmodium* extrachromosomal genetic element probe is at least 95% identical to the complement of the nucleotide sequence in the template molecule to which it hybridises. More preferably, the *Plasmodium* extrachromosomal genetic element probe is

substantially the same as the complement of the nucleotide sequence in the template molecule to which it hybridises.

Preferably, the *Plasmodium* extrachromosomal genetic element probe is contained in an aqueous mixture of other nucleic acid primer molecules. More preferably, the nucleic acid primer molecule is in a substantially pure form.

According to this embodiment of the invention, the *Plasmodium* extrachromosomal genetic element probe(s) may comprise inosine, adenine, guanine, thymidine, cytidine or uracil residues or functional analogues or derivatives thereof which are capable of being incorporated into a polynucleotide molecule, provided that the resulting probe is capable of hybridising under at least low stringency conditions to a *Plasmodium* extrachromosomal genetic element.

In a particularly preferred embodiment, the *Plasmodium* extrachromosomal genetic element probe comprises the sequence of nucleotides set forth in any one or more of SEQ ID Nos: 5-10 or a complementary strand or a homologue, analogue or derivative thereof.

In a more particularly preferred embodiment, the *Plasmodium* extrachromosomal genetic element probes are hybridised to a *Plasmodium* extrachromosomal genetic element contained in the biological sample being analysed, as probe pairs, in the combinations comprising SEQ ID Nos:5-6 or SEQ ID Nos:7-8 or SEQ ID NOs:9-10 or complementary strands, homologues, analogues or derivatives thereof.

In a most particularly preferred embodiment, the *Plasmodium* extrachromosomal genetic element probes are hybridised to a *Plasmodium* extrachromosomal genetic element contained in the biological sample being analysed, as the L/L probe pair comprising SEQ ID Nos:5-6 or complementary strands, homologues, analogues or derivatives thereof.

The *Plasmodium* extrachromosomal genetic element present in the biological sample,

or a part or fragment thereof which is enzymically-amplified, is defined herein as a "template molecule". The template molecule may be a genetic sequence which is at least 40% identical at the nucleotide sequence level to SEQ ID NOs:1-4 or to its complementary nucleotide sequence or the *Plasmodium vivax* or *Plasmodium malariae* sequences set forth in Figure 9, the only requirement being that it comprises a *Plasmodium* extrachromosomal genetic element as hereinbefore defined.

Those skilled in the art will also be aware that, in one format, the polymerase chain reaction provides for the hybridisation of non-complementary *Plasmodium* extrachromosomal genetic element probes to different strands of the template molecule, such that the hybridised probes are positioned to facilitate the 5′→ 3′ synthesis of nucleic acid in the intervening region, under the control of a thermostable DNA polymerase enzyme. As a consequence, the polymerase chain reaction provides an advantage over other detection means in so far as the nucleotide sequence in the region between the hybridised *Plasmodium* extrachromosomal genetic element probes may be unknown and unrelated to any known nucleotide sequence.

In a particularly preferred embodiment, the nucleic acid template molecule comprises, in addition to other nucleotide sequences, a sequence of nucleotides derived from or contained within any one or more of the sequences set forth in SEQ ID Nos:1-10 or a complementary sequence or a homologue, analogue or derivative thereof.

In an alternative embodiment, wherein the detection means is AFLP, the *Plasmodium* extrachromosomal genetic element probes are selected such that, when nucleic acid derived from the biological sample, in particular DNA, is amplified, different length amplification products are produced from different *Plasmodium ssp.* The amplification products may be subjected to electrophoresis, transferred to a solid support such as, for example, a nylon or nitrocellulose membrane, and hybridised to the *Plasmodium* extrachromosomal genetic element probe as hereinbefore defined, optionally labeled with a reporter molecule. According to this embodiment, a specific pattern of amplified DNA fragments is hybridised to the *Plasmodium* extrachromosomal genetic element probe, said pattern optionally specific

for a particular *Plasmodium ssp.*, to enable the user to distinguish between different species of the parasite in much the same way as for RFLP analysis.

The technique of AMD facilitates, not only the detection of a *Plasmodium* extrachromosomal genetic element in a biological sample, but also the determination of nucleotide sequence variants which differ from the *Plasmodium* extrachromosomal genetic element probe used in the assay format.

Wherein the detection means is AMD, the *Plasmodium* extrachromosomal genetic element probe is end-labeled with a suitable reporter molecule and mixed with an excess of the amplified template molecule. The mixtures are subsequently denatured and allowed to renature to form nucleic acid "probe:template hybrid molecules" or "hybrids", such that any nucleotide sequence variation between the probe and the temple molecule to which it is hybridised will disrupt base-pairing in the hybrids. These regions of mismatch are sensitive to specific chemical modification using hydroxylamine (mismatched cytosine residues) or osmium tetroxide (mismatched thymidine residues), allowing subsequent cleavage of the modified site using piperidine. The cleaved nucleic acid may be analysed using denaturing polyacrylamide gel electrophoresis followed by standard nucleic acid hybridisation as described *supra* to detect the *Plasmodium* extrachromosomal genetic element nucleotide sequences.

Those skilled in the art will be aware of the means of end-labeling a genetic probe according to the performance of the invention described in this embodiment.

According to this embodiment, the use of a single end-labeled probe allows unequivocal localisation of the sequence variation. The distance between the point(s) of sequence variation and the end-label is represented by the size of the cleavage product.

In an alternative embodiment of AMD, the probe is labeled at both ends with a reporter molecule, to facilitate the simultaneous analysis of both DNA strands.

Wherein the detection means is IRS-PCR, the *Plasmodium* extrachromosomal genetic element probes are selected such that they each include one highly-repetitive restriction enzyme cleavage site, for example *Alu*I, which is ubiquitous in many genomes. According to this embodiment, the appropriate restriction enzyme cleavage site is selected such that it is ubiquitous in *Plasmodium* extrachromosomal genetic element nucleotide sequences. The amplified template DNA is electrophoresed under conditions which facilitate high resolution and optionally probed with a labeled *Plasmodium* extrachromosomal genetic element probe.

Optionally, the amplified template DNA may be end-filled using Klenow fragment of DNA polymerase I or other suitable means, prior to the electrophoresis step.

According to this embodiment, different combinations of probes produce different patterns of amplified template nucleic acid.

Furthermore, with any probe combination used, each *Plasmodium ssp.* will produce a distinctive pattern of amplified template nucleic acid. As a consequence, the detection means is suitable for distinguishing between different *Plasmodium ssp.*, in addition to being useful for the detection of the *Plasmodium* extrachromosomal genetic element *per se* in a biological sample.

Wherein the detection means is RT-PCR, the nucleic acid sample comprises an RNA molecule which is a transcription product of the *Plasmodium* extrachromosomal genetic element DNA or a homologue, analogue or derivative thereof. As a consequence, this assay format is particularly useful when it is desirable to determine expression of one or more *Plasmodium* extrachromosomal genetic element genes.

According to this embodiment, the RNA sample is reverse-transcribed to produce the complementary single-stranded DNA which is subsequently amplified using standard procedures.

The present invention clearly extends to the use of any and all detection means referred to *supra* for the purposes of diagnosing *Plasmodium* infection in humans and other animals. Variations of the embodiments described herein are described in detail by McPherson *et al.* (1991), which is incorporated in the references.

A further aspect of the present invention contemplates a kit for convenient detection of a *Plasmodium ssp.* in a biological sample.

In an alternative embodiment, the kit of the present invention is also useful for convenient assay of infection by a *Plasmodium ssp.* parasite, wherein the sample being tested is derived from a human or other animal suspected of being infected with said parasite.

The kit of the present invention is compartmentalized to contain in a first compartment, one or more nucleic acid molecules which comprise a sequence of nucleotides corresponding to a *Plasmodium* extrachromosomal genetic element or a complementary nucleotide sequence or a homologue, analogue or derivative thereof as hereinbefore defined.

In a particularly preferred embodiment, the first compartment is adapted to contain one or more nucleic acid molecules which are at least 95% identical to the nucleotide sequence set forth in any one or more of SEQ ID Nos:1-4 or any one or more of the *Plasmodium vivax* or *Plasmodium malariae* sequences set forth in Figure 9 or its complement or a derivative, homologue or analogue thereof.

The kit optionally comprises several second containers comprising a reaction buffer suitable for use in one or more of the detection means described herein and optionally several third containers comprising a nucleic acid molecule positive standard, to which the assay sample result may be compared.

In an exemplified use of the subject kit, a negative control reaction is carried out in which the contents of the first container are contacted with the contents of the second container.

At the same time, the sample to be tested is contacted with the contents of the first and second containers for a time and under conditions sufficient for hybridisation to occur. If the reagents contained in the first container provided are not labelled with a reporter molecule, then the contents of the first container may be so labeled prior to the hybridisation reaction being carried out. The hybridised test sample and the negative control sample are then subjected to a detecting means as hereinbefore described. In analysing the results obtained using said kit, the control negative control reaction, test sample and nucleic acid molecule positive standard are compared side-by-side. The contents of the third container should always provide a positive result upon which to compare the results obtained for the negative control and test sample. If the results of the test sample are identical to the results obtained for the negative control, then the biological sample does not contain a *Plasmodium ssp.* extrachromosomal genetic element. However, if the test sample produces a nucleic acid molecule which is similar or the same as that contained in the positive standard, albeit of different intensity, then the biological sample contains a *Plasmodium ssp.* extrachromosomal genetic element.

A further aspect of the invention provides a specific extrachromosomal genetic element probe, derived from *Plasmodium ssp*, or a homologue, analogue or derivative thereof, according to the embodiments described herein.

In a preferred embodiment, the extrachromosomal genetic element probe is derived from a species of *Plasmodium* other than *P. falciparum.* More preferably, the extrachromosomal genetic element probe is derived from a *Plasmodium ssp.* selected from the list comprising *P. vivax*, *P. malariae*, *P. ovale*, *P. cynomolgi*, *P. gonderi*, *P. (Hepatocytis) kochi*, *P. inui*, *P. knowlesi*, *P. reichenowi*, *P. rodhaini*, *P. schwetzi*, *P. cathemerium*, *P. elongatum*, *P. relictum*, *P. lophurae*, *P. gallinaceum*, *P. yoelii*, or *P. berghei*, amongst others.

In a particularly preferred embodiment, the extrachromosomal genetic element probe is derived from *P. berghei*, *P.vivax* or *P.malariae*. More particularly, the extrachromosomal genetic element probe comprises a sequence of nucleotides which is at least 95% identical to

the sequence set forth in any one or more of SEQ ID Nos:1-10, or any one or more of the *P.vivax* or *P.malariae* sequences set forth in Figure 9 or a complementary nucleotide sequence, homologue, analogue or derivative thereof which is at least useful as a probe for the diagnosis of infection of a human or animal subject by a *Plasmodium ssp*.

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The present invention is further described by the following non-limiting Figures and Examples.

In the Figures:

Figure 1 is a copy of a photographic representation of an electron micrograph of the *Plasmodium berghei* extrachromosomal plasmid preparation. P donates the *P.berghei* plasmid while M is pBR322 (4.36 kb) used as a size marker. The bar represent the size of 1 kb.

Figure 2 is a copy of a photographic representation showing the *Eco*RI and *Hin*dIII restriction digests of *Plasmodium berghei* extrachromosomal plasmid DNA. In panel (a), plasmid DNA was digested with 20 units of *Eco*R I (New England Biolabs (NEB), Beverky, MA, USA) in a reaction mixture of 10 uL. The digested products were separated on a 0.4% (w/v) agarose gel at 120 V for 6 hours. Lane 1 shows Lambda Monocut markers (NEB, USA); lane 2 the *Eco*RI digest resulting in three fragments (El, E2 and E3); lane 3 shows Lambda DNA-Hind III digest markers (NEB, USA); and lane 4 shows Lambda DNA-*Bst*EII digest markers (NEB, USA). Panel (b) shows a *Hin*dIII digest of the extrachromosomal element of *P.berghei*. The digested products were separated on a 0.6 % (w/v) agarose gel at 100 V for 6 hours. Lane 1 shows Lambda DNA-*Bst*EII digest markers (NEB, USA); lane 2 shows a *Hin*dIII digest of *P. berghei* DNA resulting in six fragments (H1, H2, H3, H4, H5 and H6); and lane 3 shows Lambda DNA-*Bst*EII digest markers (NEB, USA).

Figure 3 is a copy of a photographic representation of a Southern Hybridization of *Hin*dIII and *Hin*dIII /*Eco*RI digests of the *Plasmodium berghei* extrachromosomal element. Panel (a) shows restriction digests of *P. berghei* extrachromosomal DNA. Lane M1 shows the 123 bp DNA marker (Gibco-BRL); lane HE the *Hin*dIII /*Eco*RI digest resulting in 8 fragments (H2, H3, H4, HE1, H5, HE2, E1 and E2); lane H the *Hin*dIII digest resulting in 6 fragments, H2, H3, H4, H5 and H6); lane M2 the Lambda DNA-*Hin*dIII digest markers (NEB, USA); and lane M3 the Lambda DNA-*Bst*EII digest markers (NEB, USA). Panel (b) shows a Southern hybridization of the fragments in panel (a) with probe PS 1. Panel (c) shows a Southern hybridization of the fragments in panel (a) with probe PL2. Panel (d) shows a Southern hybridization of the fragments in panel (a) with probe PSL.

Figure 4 is a representation of the physical and genetic map of the *Plasmodium berghei* circle. Panel (a) is a schematic representation of the arrangement of various genes and the *Eco*RI and *Hin*dIII sites are shown. The three *Eco*RI fragments, E1, E2 and E3 as well as the *Hin*dIII fragments Hl, H2a, H2b as well as H4 are shown. Fragment H6 comprises of HE1, E1, E2 and HE2. The relative position of the various PCR products (Table 1) is also indicated. Panel (b) shows a comparison between homologous genes on the *Plasmodium falciparum* and *Plasmodium berghei* plasmid circles.

Figure 5 is a copy of a photographic representation showing RT-PCR analysis of rRNA transcripts. Lane 1 shows the 123bp DNA ladder (Gibco BRL); lanes 2 and 3 show the RT-PCR products (L and S) using a set of *lsu-rRNA* gene specific primers and a set of *ssu-rRNA* gene specific primers respectively.

Figure 6 is a copy of a photographic representation showing PCR amplification products generated using the primer set L1/L2 (SEQ ID NO: 5/SEQ ID NO: 6) (Panel a), and the primer set DHFR1/DHFR2 (Panel b). Blood was drawn daily for 5 days from a mouse initially infected with 5 x 10^4 parasites. Lanes 1-5 in both panels show the amplification products obtained from blood spots 1 to 5 days post-infection correspondingly. Lane 6 is the negative control with blood from an uninfected mouse and lane 7 is the positive control using 50ng of purified *P.berghei* total DNA as template. M indicates the 100bp DNA ladder (Promega) used as markers.

Figure 7 is a copy of a photographic representation showing PCR amplification of blood spots from Laotian patients diagnosed positive for *P.falciparum* malaria by Giemsa microscopy and ParaF dipstick, with the exception of one which was infected with *P. vivax* (lane 11). Primers used were the L1/L2 primer set (i.e. SEQ ID NO: 5/SEQ ID NO: 6). Lane 12 is the negative control with a blood spot from a healthy person and lane 13 is the positive control using 50ng of purified *P.falciparum* (FC27 strain) total DNA as template. M indicates the 100bp DNA ladder (Promega) used as markers.

Figure 8 is a copy of a photographic representation showing PCR amplification of blood spots from uninfected persons using the L1/L2 (SEQ ID NO: 5/SEQ ID NO: 6) primer set (Panel a) and AC1/AC2 primer set (Panel b). Lanes 1 and 2 are positive controls for human β-actin using 50ng of purified total DNA from CaSki and HeLa cells. Lanes 3-10 use blood spots from uninfected persons as the template. Lanes 11 and 12 in (a) use blood spots from a *P.falciparum*-infected patient and a *P.vivax*-infected patient respectively. M indicates the 100bp DNA ladder (Promega) used as markers.

Figure 9 is a copy of a schematic representation of the aligned LSU-rRNA sequences from different *Plasmodium* species obtained from various regions in Asia. The alignment was carried out using the Clustal Method in the DNASTAR programme. Sequences indicated are derived from several isolates of *P.falciparum* (Pf), *P.vivax* (Pv), *P.malariae* (Pm) or *P.berghei* (Pb). The alphanumeric designation following the *Plasmodium* species descriptor indicates the isolate number and geographical origin of the specimen, wherein P=Pakistan, I=India, L=Laos and S=Singapore. The GenBank accession numbers for Pf(C10) and Pb(ANKA) are X95275 and U79731 respectively. Boxes indicate residues which differ from the C10 sequence (basepair 4110-4704).

EXAMPLE 1

Preparation of *Plasmodium berghei* extrachromosomal DNA

Plasmodium berghei (ANKA strain) was maintained in Swiss White mice by continuous blood passage. Development of parasitemia was monitored daily by thin blood film analysis (Shute, 1988). Parasites were obtained by lysis of infected red blood cells with 1% saponin. The extrachromosomal element was purified from the parasites using a modified procedure of the Qiagen plasmid mini preparation kit (Qiagen Inc., Chatsworths, CA, USA). Parasites from 10 infected mice (20-25 g) with a parasitemia of 60% were resuspended in 5 ml of P1 buffer, lysed with 5 ml of P2 buffer and neutralised with 5 ml of P3 buffer. After chilling on ice for 20 minutes, the precipitate was removed by centrifugation according to the manufacturer's recommendation and 200 μl of proteinase K (50 mg/ml) were added to the supernatant, which was then reincubated for 2 hours at 37 C. The supernatant was subsequently passed through a tip-20 Qiagen column which had previously been equilibrated with 1 ml of QBT buffer. The column was washed four times with 1 ml of QC buffer each. Finally, the extrachromosomal element was eluted with 1 ml of QF - buffer which was preheated to 65 C. The DNA was precipitated with isopropanol, washed with 70% ethanol, dried and dissolved in 25 μL of TE buffer.

EXAMPLE 2

Preparation and restriction digest of *P. berghei* extrachromosomal DNA

Plasmodium berghei extrachromosomal DNA was extracted from the parasite using the Qiagen plasmid mini preparation kit (Qiagen Inc., Chatsworths, CA, USA). Electron microscopic analysis of this preparation showed circular DNA elements of about 10 times the size of control pBR 322 plasmids (Figure 1). The preparation was not homogenous and, in addition to the circular elements many linear molecules of different lengths were observed. The preparation is enriched for the extrachromosomal DNA elements of both circular and

linear DNA representing the homologues of the 35 kb circle and 6 kb mitochondrial DNA. These are likely to be 6 kb DNA molecules which are tandemly arrayed in head-to-tail configurations.

The extracted plasmid DNA was digested into 3 fragments of 15 kb (E3), 10 kb (E2) and 5.7 kb (E1) by *EcoR* I (Fig. 2a). This gives the plasmid an estimated size of 31 kb. *Hind* III digest of the DNA yielded 6 fragments of 22.4 kb (H6), 4.4 kb (H5), 1.85 kb (H4), 1.23 kb (H3), 0.95 kb (H2) and 0.7 kb (H1), respectively (Fig. 2b).

The estimated size of the *P. berghei* circle is 31 kb according to Electron microscopic measurements using pBR322 as control as well as from size calculations using the *EcoR* I restriction digest fragments.

Extrachromosomal circular DNA has not only been found in *Plasmodium* species but also in other parasitic protozoa such as *Babesia* and *Entamoeba* (Gozar and Bagnara, 1995; Egea and Lang-Unnasch, 1995; Sehgal et al., 1994) suggesting a common evolutionary origin of this circular DNA material (Williamson et al. 1994). By maintaining such extrachromosomal information during evolution it appears that this highly conserved and seemingly functional extrachromosomal DNA molecule is important for parasite development and that knowledge of its functions will greatly aid in providing novel targets for drug development.

Our preliminary tests using an antisense oligonucleotide approach indicate that this extrachromosomal element may indeed be crucial for parasite survival.

EXAMPLE 3

PCR amplification and sequence analysis of plasmid DNA.

In order to obtain a genetic map of the *Plasmodium berghei* extrachromosomal plasmid, polymerase chain reaction (PCR) amplifications and sequence analysis of plasmid

DNA were carried out.

PCR was performed using the United States Biochemical (Amersham) PCR kit in a 100 μl reaction mixture containing 2 mM $MgCl_2$, 0.2 mM of each dNTP, 4 ng/μL of each primer, 5 units of *Taq* DNA polymerase, 10 μL of the 10 X PCR buffer and 1 μL of the extrachromosomal DNA prepared as described in Examples 1 and 2. A "hot start" was carried out at 95°C for 5 minutes without the dNTPs and Taq polymerase. This was followed by the addition of dNTPs and Taq polymerase and 40 cycles of denaturation (90°C, 1.5 minutes), annealing (55°C, 3 minutes) and extension (72°C, 5 minutes). A final extension was performed at 72°C for 10 minutes.

The PCR products were loaded onto a 1 % low melting point agarose gel, extracted by the freeze-thaw method (Shoemaker and Slayers, 1991) and then cloned into the Promega pGEM-T vector.

Clone H2a was constructed by cloning the second fragment of a *Hin*dIII digest of the extrachromosomal element into the pBluescript vector. (Stratagene, USA).

The clones were sequenced using the ABI PRISM Dye terminator cycle sequencing kit from Perkin-Elmer on the 373A DNA sequencer from Applied Biosystems. The percentage homology with the P. falciparum extrachromosomal element (Accession No. X 95275 and X 95276) was obtained using the Martinez/Needleman-Wunsch DNA alignment programme from DNASTAR.

PCR amplification of different parts of the extrachromosomal plasmid were performed using primer sets homologous to sequences from the 35 kb circle of *P.falciparum* (Table 1). These include the primer sets comprising SEQ ID Nos:5 and 6 (L/L Primer set), SEQ ID Nos:7 and 8 (L/S primer pair) and SEQ ID Nos:9 and 10 (S/S Primer pair, homologous to the small-subunit (ssu) -*rRNA* of *P. falciparum*).

The amplified regions obtained with these primers lay within the large subunit (lsu) -*rRNA* gene, *rpo B* gene, the cluster of 10 *tRNAs*, part of the cluster of four *tRNAs* located close to the 3' end of the *tufA* gene in *P. falciparum* as well as the region between the *lsu-rRNA* and the *ssu-rRNA* genes.

All PCR fragments were cloned into the pGem-T vector from Promega. Sequence analysis performed using the Martinez/Needleman-Wunsch DNA alignment on all clones which had been purified using Qiagen midi plasmid preparation columns showed a similarity index of greater than 80% with the *P.falciparum* circle except for the PPH and PWQ fragment (Table 1). The PRB fragment was homologous to the *P.falciparum rpo B* gene with a similarity index of 87.9% for the DNA sequence and 85.6% for the corresponding amino acid sequence (using the Lipman-Pearson protein alignment). The PPH sequence spanning the cluster of 10 *tRNA* genes had a similarity index of only 78%. While the *tRNA* coding regions were highly similar to those in *P.falciparum* the non-coding spaces were much less conserved between the two Plasmodium species.

In order to examine if the *lsu-rRNA* gene in *P. berghei* exists as a repeat, a single forward primer (L3) homologous to the 3' end of the *P.falciparum lsu-rRNA* sequence and 2 distinct reverse primers homologous to the ORF 470 (04) and the start of the cluster of 10 *tRNA* genes (3H) of the *P.falciparum* circle were designed. The fragment amplified with the L3/04 primer set (PL470) was distinct from that amplified using the L3/3H set (PLH). Sequence analysis of PL470 showed a homology of 83% with the same region in *P. falciparum*. The sequence of PLH was homologous to the 3' end of the *lsu-rRNA* and the 3' end of *rps 4* of the *P.falciparum* circle (data not shown) indicating that the *lsu-rRNA* gene exists as a repeat in *P.berghei*. In addition, a cluster of intervening *tRNA* genes was present between the *lsu-rRNA* and *ssu-rRNA* genes (fragment PLS). This repetition and arrangement is similar to the organisation of the *P.falciparum* circle, where a palindromic sequence of genes for the subunit *rRNAs* and several *tRNAs* exists. Each arm of the palindrome contains one *ssu* and one *lsu-rRNA* gene and a cluster of intervening *tRNA* genes (Gardner *et al.*, 1993).

From the nucleotide sequences set forth in SEQ ID NOs:1-4, it is clear that the genes in the *P.berghei* circle are homologous to those in the 35 kb *P.falciparum* circle. Major differences in sequence are observed in the non-coding spaces between tRNA gene clusters. The arrangement of genes appears to be similar in both Plasmodium species and a repeat of the rRNA genes does not only exist in *P.falciparum* but also in the *P.berghei* circle.

EXAMPLE 4

Southern Hybridisation of restriction fragments

Fragments from the *Hin*dIII and *Hin*dIII/ *Eco*RI digests of the *Plasmodium berghei* extrachromosomal element were separated on a 1 % (w/v) agarose gel at 120 V for 4 hours. The separated fragments were then transferred onto a Nylon membrane (Hybond-N, Amersham) by capillary action using 20x SSC buffer (0.3M sodium citrate, 3M sodium chloride, pH 7.0). Southern hybridization was performed using probes that were made from the cloned PCR products, according to the preceding Examples.

The PCR products were liberated from the vector by digestion with *Apa*I and *Pst*I. The enhanced chemiluminescence (ECL) direct nucleic acid labelling and detection system (Amersham International PLC, England) was used for labelling the probe, for hybridisation and for detection.

Table 1. Description of clones of various segments from the extrachromosomal element in *P. berghei* and their percentage homology with *P. falciparum*.

Name of clone	Description	Size (bp)	Percentage homology with *P.falciparum*	*EcoRI*/*HindIII* sites
H2a	Second fragment of *HindIII* digest containing SSU rRNA	949	92.3	*HindIII* 1, 944
PS1	PCR product of SSU rRNA	526	94.3	Nil
PL.	PCR product of LSU rRNA	595	95.5	*HindIII* 113
PL2	PCR product of LSU rRNA	554	92.7	*HindIII* 575
PL3	PCR product of LSU rRNA	735	88.8	*HindIII* 177
PLS	PCR product of tRNAs between LSU and SSU rRNA	973	87.3	Nil
PPH	PCR product of tRNAs before the repeat	1000	78.0	*Eco*RI 105
PLH	PCR product from LSU rRNA to HtRNA	1118	82.3	Nil
PL470	PCR product from LSU to ORF470	1125	83.0	Nil
PRB	PCR product of the RpoB gene	516	87.9	*Eco*RI 273
PWQ	PCR product of the Phe and Gly tRNAs	161	69.6	Nil

Each of these steps were carried out according to the manufacturer's instruction. First, 8 μg of probe in a volume of 20 μL were denatured by boiling for 5 minutes and immediately cooled on ice for 5 minutes. 20 μL of labelling reagent were then added. This was followed by the addition of 20 μL of glutaraldehyde solution. The mixture was incubated for 20 minutes at 37°C before addition to the hybridization buffer. The ECL Gold hybridisation buffer containing O.5M NaCl and 5% blocking agent was used for hybridisation. The blots were prehybridised for 2 hours at 42°C and the labelled probe was added to a final concentration of 800 ng DNA/ml. Hybridisation was allowed to proceed overnight at 42°C. The blots were washed twice in primary wash buffer containing 6M urea, 0.4% SDS and O.5x SSC at 42°C for 20 minutes. This was followed by two rounds of washing in 2x SSC buffer at room temperature for 10 minutes. For detection, 6.5 ml of equal volumes of detection reagents 1 and 2 were mixed and added to the blot for 1 minute. The blot was then drained, wrapped in Saran Wrap and the DNA side was exposed to an autoradiography film.

A double digest of the *P. berghei* circle with *Hin*dIII followed by *Eco*RI resulted in the following fragments: 10kb (E2), 5.7kb (E1), 5.0kb (HE2), 4.4kb (H5), 2.3kb (HE1), 1.85 (H4), 1.23 (H3), 0.95(H2) and 0.7kb (H1). The PS 1 probe hybridised to H2, the PL. probe hybridised to H6 and HE2 while the PWQ probe hybridised to H6 and H2 (Fig. 3).

The results obtained with various other probes are shown in Table 2. Of interest to note is that H2 contained 2 distinct fragments which hybridised with PS 1 and PL3. One of the H2 fragments (H2a) was cloned into Bluescript vector (pBS KS (II)+) and sequenced. The sequence corresponded to the internal region of the *P.falciparum* 35 kb ssu-rRNA gene (Table 1, sequence H2a). The other fragment (H2b) arose from the two Hind III sites within the lsu-rRNA gene. The presence of these two sites was confirmed by the sequences from the PL2 and PL3 PCR products. In addition, both the H5 and the H3 fragments hybridised with probes corresponding to the *P.berghei* 6 kb mitochondrial DNA. This was not unexpected as the preparation was found to contain linear molecules as shown by electron microscopy (Fig. 1).

Table 2. Southern analysis of restriction digests.

Probe	*Hind*III digest	*Hind*III/*Eco*RI digest	*Eco*RI digest
PS1	H2	H2	N.D.
PLS	H4	H4	N.D.
PWQ	H6	E2	E2
PL.	H6	HE2	N.D.
PL2	H6	HE2	N.D.
PL3	H2, H4	H2, H4	E3
PRB	H6	HE2	E2, E3
PL470	H6	HE2	E3
PPH	H6	HE1	E3
PbIV2.3	H3, H5	H3, H5	N.D.

EXAMPLE 5

Physical and genetic map

A map of the *P. berghei* extrachromosomal circle was constructed based on the information from the restriction digests, Southern hybridisation experiments and the sequence analysis of the PCR fragments (Fig. 4a). The PPH and PRB fragments each contained an *EcoR* I restriction site (Table 1). The three *EcoR* I and six *Hind* III fragments were arranged according to their hybridisation patterns. The PRB probe hybridised to both the E2 and E3 fragments from the *EcoR* I digest indicating that E2 is positioned next to E3 (Table 2).

The HE2 fragment obtained from the double digest with *EcoR* I and *Hind* III, hybridised to probes PRB, PL470 and PL2 while H2b and H4 hybridised to probe PL3. Both the PL2 and PL3 fragments are regions within the *lsu-rRNA* gene, whereas the PL470 fragment contains 3' end of the *lsu-rRNA* gene. Thus, the ORF470 must be located next to the PL2 fragment. H2b is situated between HE2 and H4 since H4 also hybridised with the PLS probe which contains the 5' ends of both the small and large subunits rRNA genes. H2a hybridised with probe PS 1 which corresponds to a region within the ssu-rRNA gene, therefore H2a must be located next to H4. Finally, HE1 is placed next to E1 as HE1 hybridised to probes PPH, PLH and PL2.

The arrangement of genes on the *P. berghei* circle spanning the *rpo B* gene and the cluster of 10 *tRNAs* genes is thus very similar to that of the *P.falciparum* 35 kb circle (Fig. 4b). The *P.berghei* circle encodes organelle-like rRNAs, tRNAs, ribosomal proteins and RNA polymerase subunits, similar to those identified for *P. falciparum* (Preiser *et al.*, 1995).

EXAMPLE 6

Reverse transcription-PCR of LSU-rRNA and SSU-rRNA

In order to determine if the *Plasmodium berghei* extrachromosomal genetic element is transcriptionally active, total RNA from *P. berghei* was isolated using the RNeasy total RNA kit (Qiagen Inc., Chatsworth, CA, USA) and a combined reverse transcription - PCR (RT-PCR) reaction was carried out to amplify *lsu-rRNA* or *ssu-rRNA* transcripts.

Total RNA was isolated from *Plasmodium berghei* using the Qiagen RNeasy Total RNA kit (Qiagen Inc., Chatsworth, CA, USA). Parasites from 10 infected mice with a parasitemia of 60% were resuspended in 350 μl of lysis buffer RLT and homogenised using a QIAshredder (Qiagen Inc.). The homogenate was cleared of insoluble material by centrifugation and 1 volume of 70% ethanol was added. The entire sample was then added to the RNeasy spin column and washed with RW1 buffer followed by two washes with RPE buffer. The RNA was eluted out with 35 μl of water. 5 μl of the RNA was used as starting material for the Access RT-PCR system (Promega, Madison, USA). Two primer sets, L/L (SEQ ID Nos:5 and 6) and S/S (SEQ ID Nos:9 and 10) were used. The manufacturer's protocol was followed with the exception of the annealing step for PCR amplification. Annealing was allowed to proceed at 55°C for 1 minute. The PCR products were separated on a 1% (w/v) agarose gel and visualised by ethidium bromide staining.

Amplification using the RT- PCR kit from Promega and a set of primers homologous to the ssu-rRNA produced a 526 bp fragment while amplification using a set of *lsu-rRNA* specific primers resulted in a 600bp fragment (Fig. 5).

EXAMPLE 7

Assay of blood samples for the presence of *Plasmodium ssp.*

A total of 102 *Plasmodium*-infected blood samples from four different locations, Singapore, Laos, Karachi and Calcutta, and a defined number of negative control blood samples, were analysed for the presence of *Plasmodium* extrachromosomal genetic elements, using the polymerase chain reaction.

Briefly, 10-100μL of whole patient blood (either peripheral blood from a finger prick sample or venal blood) was spotted onto a filter disc or equivalent solid support and directly amplified, using each of the primer pairs:

L/L PRIMER PAIR:

SEQ ID NO:5:	5'-GACCTGCATGAAAGATG-3'
SEQ ID NO:6:	5'-GTATCGCTTTAATAGGCG-3'

L/S PRIMER PAIR:

SEQ ID NO:7:	5'-GCCACTACTATGAAAATC-3'
SEQ ID NO:8:	5'-GCGTTCATTCTGAGCTAG-3'

S/S PRIMER PAIR:

SEQ ID NO:9:	5'-GCGGTAATACAGAAAATGCAAGCG-3'
SEQ ID NO:10:	5'-AGCACGAACTGACGACAGCCATGCAC-3'

PCR Buffer used in the amplification reactions comprised the following:

70mM Tris. pH8.8

20mM Ammonium sulphate

1 mM DTT

0.1μg/μL BSA

2.5mM $MgCl_2$

Each 100 μL reaction included 0.4μg of each primer, 0.8mM dNTP mixture and 5U of *Taq*I polymerase.

The template DNA was fixed with methanol for 5 mins. A "hot start" was carried out at 95°C for 5 minutes without the dNTPs and Taq polymerase. This was followed by the addition of dNTPs and Taq polymerase and 40 cycles of denaturation (90°C, 1.0 mins), annealing (60°C, 2 mins) and extension (72°C, 3 mins). The PCR products were analysed by agarose gel electrophoresis.

The results are shown in Tables 3 and 4. The L/L primer set was capable of identifying *Plasmodium falciparum, P. vivax* and *P. malariae* in 100% of cases, suggesting that this primer pair is useful in the genera-specific diagnosis of *Plasmodium* infection. The S/S primer set was capable of efficiently diagnosing *P. falciparum* and *P. malariae* in 100% of cases. In marked contrast, the L/S primer set resulted in only poor diagnosis of *P. vivax* and *P. malariae*, however detected the presence of *P. falciparum* in blood samples, suggesting that this primer pair is species-specific.

Results also indicate that the selection of primer pairs in the diagnostic assay was of primary importance in determining the reliability of the assay in diagnosing infection by *Plasmodium ssp.*

TABLE 3

Number and origin of *Plasmodium*-infected blood samples

ORIGIN	TOTAL No. OF SAMPLES	*Plasmodium falciparum*	*Plasmodium vivax*	*Plasmodium malariae*
Singapore	13	7	5	1
Laos	11	10	1	0
Karachi	67	14	53	0
Calcutta	11	1	10	0
TOTAL	102	32	69	1

TABLE 4

PCR results using the primer pairs L/L, L/S and S/S

Plasmodium ssp.	L/L Primers	L/S Primers	S/S Primers
P. falciparum	32/32 (100%)	14/20 (70%)	21/21 (100%)
P. vivax	69/69 (100%)	6/58 (10%)	48/57 (84%)
P. malariae	1/1 (100%)	0/1 (0%)	1/1 (100%)
TOTAL	102/102 (100%)	20/79 (25.3%)	70/79 (88.6%)

EXAMPLE 8

Direct PCR amplification of extrachromosomal *Plasmodium* DNA from dried blood spots

1. *Specimen Collection*

Blood was collected by fingerprick (5-10 μl) or by venipuncture from subjects with Giemsa smear-positive *Plasmodium falciparum*, *Plasmodium vivax* and *Plasmodium malariae* malaria as well as from healthy controls, and spotted in replicates onto Whatman filter paper. *Plasmodium berghei* (ANKA) infected mouse blood (5μl) was collected from the tail. *Plasmodium berghei* infections were maintained by serial blood passage of 10^7 parasites. Dried blood spots were placed individually into 200μl PCR tubes and fixed with the addition of methanol for 5 minutes. The methanol was poured off and the blood spot was dried thoroughly prior to PCR amplification.

2. *PCR amplification*

Amplification was carried out as previously described (Long *et al*, 1995) with some modifications. Each 100μl reaction mixture contained 1xPCR buffer (70 mM Tris, pH 8.8, 20 mM $(NH_4)_2SO_4$, 1 mM DTT, 0.1 μg/μl BSA) 2.5 mM $MgCl_2$, 0.4μg of each primer, 5 units of Taq DNA polymerase (Amersham) and 0.2 mM of each dNTPs. Reaction tubes were overlaid with one drop of mineral oil. The reaction was soaked at 95°C for 5 minutes then held at 80°C prior to the addition of Taq DNA polymerase and dNTPs. Amplification involved 40 cycles of 1 minute denaturation at 90°C, 2 minute annealing at 52°C and 3 minutes primer extension at 72°C. A 5 minute primer extension at 72°C was included following the final cycle.

3. *Sequences of primers.*

Three sets of primers were used in this study. The primers used for amplifying the LSU-rRNA gene were L1 5′ GAC CTG CAT GAA AGA TG3′ (SEQ ID NO: 5) and L2 5′GTA TCG CTT TAA TAG GCG3′ (SEQ ID NO: 6). A second set of primers designated as DHFR1 (5′GCA ATA TGT GCA TGT TGT AAA3′) and DHFR2 (5′ATT CTT TAT

AAA CAG ACG3′) were designed to amplify the dihydrofolate reductase-thymidylate synthase (DHFR-TS) gene from *P.berghei* genomic DNA in control experiments. The primers used for amplifying the human β-actin gene were AC1 (5′GGG CGA CGA GGC CCA GAG C3′) and AC2 (5′GCA TCC TGT CGG CAA TGC C3′).

4. *Agarose gel electrophoresis*

10 μl of each PCR product was resolved in 1% agarose gels with TAE electrophoresis buffer (40mM Tris-acetate and 1mM EDTA, pH 8.0). Electrophoresis was carried out at 100V for 1.5 hours and the fragments were visualized under UV.

5. *DNA sequencing protocol*

The PCR products were loaded onto a 1% (w/v) low-melting point agarose gel and extracted by the freeze-thaw method (Shoemaker and Salyers, 1990). They were then cloned into the pGEM-T vector (Promega). The clones were sequenced using the ABI PRISM Dye terminator cycle sequencing kit (Perkin Elmer) on the 373 DNA sequencer from Applied Biosystems. Multiple sequence alignment using the cluster method was carried out with the DNASTAR programme.

6. *Results*

6.1 *Detection of P.berghei infection in blood spots*

Conditions for the PCR amplification of *P.berghei* infected mouse blood spotted on filter paper were optimised using DHFR1 and DHFR2 primers. Once these conditions were established, the sensitivity of the LSU-rRNA primer set was compared with that of the DHFR-TS primer set. The LSU-rRNA primer set was designed to amplify a 594bp fragment from the *P.berghei* circular DNA while the DHFR-TS primer set amplified a 511bp fragment from *P.berghei* genomic DNA. Blood spots were prepared daily for 5 days from a mouse which was initially infected with 5 x 10^4 parasites. Giemsa staining of thin blood films from the same animal was done daily. The LSU-rRNA primer set was more sensitive than the DHFR-TS primer set in detecting parasite DNA. The amplified LSU-rRNA fragment was detectable by ethidium bromide staining one day after infection (Figure 6a) while the DHFR-

TS PCR product was only visible two days post-infection (Figure 6b). At these two time points, no parasite was detected on the corresponding Giemsa-stained blood films. Parasites were only observed on the film three days post-infection.

6.2 *PCR amplification of blood spots from malaria infected patients.*

The above PCR amplification protocol was also applied to blood spots from 31 malaria-infected patients. 15 of these samples were obtained from patients admitted to the National University Hospital in Singapore. Of these, 7 had *P.falciparum* infection, 1 had *P.malariae* and the remaining had *P.vivax* as determined by Giemsa and Quantitative Buffy Coat (QBC) diagnosis. All samples were positive for amplification with LSU primers (data not shown). The other 16 samples were from patients in Laos with 15 *P.falciparum* infections and one *P.vivax* malaria infection as determined by Giemsa diagnosis. LSU-rRNA PCR amplifications were positive for all 16 specimens. As shown in Figure 7, the PCR products from 11 of the 16 Laotian specimens. Eight healthy persons and total DNA from two human carcinoma cell lines, CaSki and HeLa were used as controls. These were all negative when using the LSU-rRNA primer set for PCR amplification but were all positive for human β-actin (Figure 8, compare panels a and b).

EXAMPLE 9

Sequence alignment of LSU-rRNA extrachromosomal DNA from various *Plasmodium* species

The LSU-rRNA fragments amplified from the blood spots as described in Example 8 were cloned into the pGEM-T vector and sequenced. In addition to amplified products from the Singaporean and Laotian patients, we also amplified and sequenced LSU-rRNA fragments from Indian and Pakistani patients. The published *P.falciparum* sequence (C10 strain) was used as the basis for all alignments and comparisons.

Comparison of the *Plasmodium* species used in this study showed that this region of the LSU-rRNA gene is highly conserved and the similarity between *P.falciparum*, *P.vivax*,

P.malariae and *P.berghei* is greater than 92% (Table 5). The similarity between the C10 and other *P.falciparum* sequences ranged from 98.3%-99.8%, while that between the C10 and the *P.vivax* sequences ranged from 92.9- 99.7%. The greatest divergence in sequence was observed from the two *P.vivax* specimens from Pakistan. In all cases, divergence in sequence was due to 1 or 2 base changes in isolated regions within the LSU-rRNA fragment (Figure 9).

TABLE 5

Percent homology of LSU-rRNA sequences with *P.falciparum* (C10 strain) sequence

Name of sequence[1]	Similarity Index to Pf(C10)[2]
Pf10/P	98.3
Pf11/P	98.5
Pf19/I	99.7
Pf20/L	99.7
Pf18/S	99.8
Pv12/P	93.4
Pv13/P	92.9
Pv15/I	99.5
Pv16/L	99.7
Pv17/S	93.4
Pm1/S	93.2
Pb(ANKA)	94.2

[1] Pf denotes *P.falciparum*, Pv denotes *P.vivax*, Pm denotes *P.malariae* and Pb denotes *P.berghei*. The alphabet at the end of each name indicates the origin of the specimen; P=Pakistan, I=India, L-Laos and S=Singapore. The GenBank accession numbers for Pf(C10) and Pb(ANKA) are X95275 and U79731 respectively.

[2] Similarity index obtained using the Martinez-Needleman-Wunsch DNA alignment programme.

EXAMPLE 10

Discussion

In this study, we have shown that it is possible to amplify the extrachromosomal circular plastid-like DNA found in *Plasmodium ssp.* This has allowed us to proceed with characterising the LSU-rRNA gene from the circular DNA of malaria-infected patients using only a small volume of blood spotted on filter paper.

We have designed a pair of primers based on the sequences from *P.falciparum* and *P.berghei* such that the primers are completely homologous for both species. Using these primers, we have been able to amplify the corresponding LSU-rRNA fragment from *P.falciparum*, *P.vivax*, *P.malariae* and *P.berghei* infected blood. Sequence analysis of these fragments indicates that this region of the LSU-rRNA is highly conserved between different species of *Plasmodium*. In addition, different geographic isolates of *P.falciparum* and *P.vivax* from Asia do not show distinct variations for the LSU-rRNA fragment. GenBank searches indicate that this fragment sequence is unique.

The high homology between the various *Plasmodium* species has led us to examine if the LSU-rRNA specific primers are useful for the detection of malaria infections. Using *P.berghei*, the LSU-rRNA primer set was shown to be more sensitive than the DHFR primer set in parasite detection in mouse blood spots. All 31 patient blood spots tested were positive regardless of the *Plasmodium* species involved while none from healthy persons was positive. These results indicate that the LSU-rRNA primers may be useful for the diagnosis of malaria infection.

The east of direct PCR amplification of extrachromosomal *Plasmodium* circular DNA from dried blood spots has provided us with the means to study and characterise the genes present on this DNA molecule. To date, none of the genes on the circular DNA of *P.vivax* and *P.malariae* has been described. This is the first description of an analysis of the LSU-rRNA gene from different field isolates of *P.vivax*, *P.malariae* and *P.falciparum*. More

investigations are being carried out to determine the extent of sequence conservation and arrangement of the genes on the circular DNA from different *Plasmodium* species.

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

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SEQUENCE LISTING

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5849 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TAAAGGATAT TTTAAAATAA CGTCCAATAA AGACAAAAAT ATAATACCTA ATTTTTTTAA 300

AAAATATTGT GTTGTATGTA AAACAGATAT ACTATCACAA ATAACATCAA TAGGAATTAT 360

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CAAATTACTA TCTTTTAAAG TAGAAGAATA ATAAATAATA TTATCATAAC TAATATTGGG 480

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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ACTTGAACTC AGAACCATTC GATTAAAAGT CGAGTACTCT ACCAATTAAG CTAGTAATTC 240

TTAATATAAC GAATCTGACG AGAATTGAAC TCGTATTCTT TGTTATGACA AAATAATATT 300

TTAACCTAAT TAAACTACAA ATTCAAATAA ATATATATAG GGAAAAGGGA TTCGAACCCT 360

GGTATATATA ATATCTACAT AAATGTAGCA ATTTATAGCT ATAACCACTC AGCCATTTCT 420

GTATATAATA ATAAGTTAAA TCAGATTGAA CTGATGTAGA TATAAAACCC AATGGATTTA 480

CAGTCCATCC CTTTTAACCC CTCAGGCATT AACTTTATTA TACATTTAAG TAGATTCGAA 540

CTACTGATGT TCAATATTTG AAAATGAATT ATGAGTCCAT TGCTTTCGAC CTCTTAGCTA 600

TAAATGTTTA CTTTATTAGA GATAAAGGGA CTCGAACCCT TACAACAATT ATTGTTAATG 660

GATTTTCTAA TTGAAATTTA GACTTTTTAT AAACATGTAT ATAAATAATA AAGTCGTTTG 720

AATATATAAC TAATATATTA CAGAATAAAA ATTATTTTTT CTTTATATAT ATTTAAATTA 780

TTAATTTATT TATAAAATTA ACTCATAAAC AACGAATATA AATTATATTT ATATTATTTA 840

AAGTCCATTG TGTATACCAA ATTTCACCAT ATCTCTATTA TATACTATAT AAATGATATT 900

CAGATTTGAA CTGAAATAAA ATAATTTGCA ATTATCCACT TTACCTAATT AAGTTATATC 960

ATTATTATAT ATTATAAGAT AAATAAAGAG ATTTGAACTC ATATAAAAGA AACCACAATT 1020

CCTTATCTTA ACCTTTAGGA TTATATTTAT CATTATTAAA ACTTATTATA TATTATAAAT 1080

ATTATTATAA ATATATAAAA TATTATTTAA ATATAAATCA TTTAATATTT TTATTTTAAA 1140

ATTATATATA CATATAATAA AATTATCATT AAAACTAGAA GATTTAATAA AATTATATTT 1200

ATATAAATTT GATATATAAA TATATATATT ATATCTATAA ATTAAATTTG GTGAAATTAT 1260

ATATTTAATT TTTTTATTAA AAAAAATTAT ATCCTTACCC TTTAATTTAA TATTATAATA 1320

ATTACCATAA ACCTTATTTA AATATACATA TTTATACCTT ATATAATATC TCAGAGTGGT 1380

GTATAGTTTT AAAAACCCCA TATTAACTAA AAAGACATCT AATCTAGGTT CTAATAGATT 1440

TAATAATTTG AGATATAAAT GATTCTCATG GTGACTCTGT ATTTTTTTCA AATAATGTAA 1500

ATATGGTTTA AATGTTATAC CATAATTATA ACAGATATAT CTTACAAATT TTAATTTTAA 1560

ATCGAAATAA GATTGATAGA CATATTTATT AATTTTTAAT TTATAATTAT ATTTACTAGA 1620

TAAATATAAT AAAAAAGGAA GATTTAATTT TTTTAACATT TTTATTTTAG GAGTTAAAAA 1680

TTTTATCATA ATAATTTTAT ATTATAAAAT A 1711

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Plasmodium berghei

(vii) IMMEDIATE SOURCE:
(B) CLONE: CLONE PRB

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTAATAGACA TGGACATAAA GGTGTTATTT CTTATATTAA TGATATTAAT GATATGCCTT 60

ATTTAAATAA CAAAATACAA CCTGATTTAT TTGTAAGTGC TATTGGTATA CCTTCTAGAA 120

TAAATATAGG TCAAATATTA GAGGGTATAT ATGGATTAAA TAGTTTATAT TTAAATAATA 180

GATATATAAT ATCTAATAAT TTAAATACTA ATTATTATAA TAATTATATT AATAATTTTA 240

ATTATTATAA ATATAATTAT AATAATAATT TTGAATTCAA TAAAATATCA TATAATTATA 300

ATAAATATTT TTTAAAAAAT CCGTTTACGG GCCATTTAAT ACAGAATAGT ATTTGTTTAA 360

ATAATATTTA TTATTATAAA TTAGTACATA TGGTAAAAGA TAAATTAAGA TATAGATTCA 420

TAGGATTATA TTCTGAATTA ACTCAACAAC CTGTAAAAGG AAATACAAAA CAAGGAGGTC 480

AAAGATTTGG TGAAATGGAA GTATGGGCGC TAGAAG 516

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Plasmodium berghei

(vii) IMMEDIATE SOURCE:
(B) CLONE: CLONE PWQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTCAAAAAT CAGATTTGAC TGATAACACA TGGAACTTCA ATCCATTGCT CTACCATTGA 60

GCTATAATGA CTTAATAATA TTATTATTAT AATAGAATAT AACCAAAAGG TTAAGGTAAT 120

GAACTTTGAT TTCATTAATA TAGGTTCGAA TCCTTTAGGA C 161

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCTGCATG AAAGATG 17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTATCGCTTT AATAGGCG 18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCACTACTA TGAAAATC 18

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTCATTC TGAGCTAG 18

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGGTAATAC AGAAAATGCA AGCG 24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCACGAACT GACGACAGCC ATGCAC 26

DATED this TWENTY FIRST day of APRIL, 1997
The National University of Singapore
by DAVIES COLLISON CAVE
Patent Attorneys for the Applicants

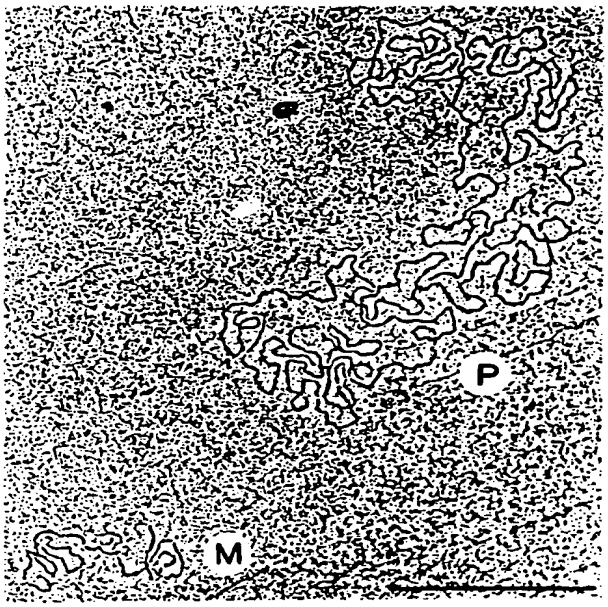

FIGURE 1

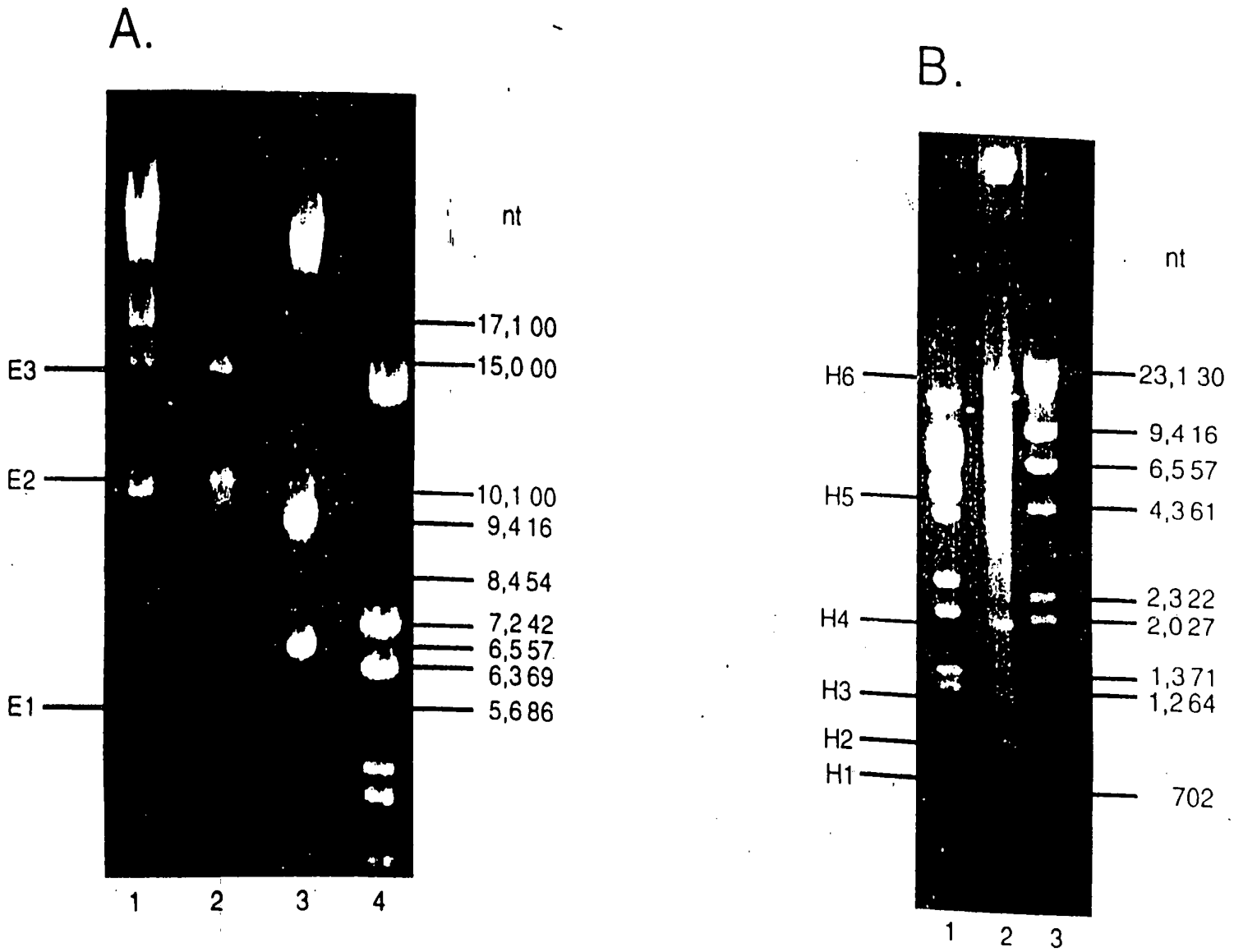
A.
nt
17,1 00
15,0 00
10,1 00
9,4 16
8,4 54
7,2 42
6,5 57
6,3 69
5,6 86
E3
E2
E1
1
2
3
4
B.
nt
23,1 30
9,4 16
6,5 57
4,3 61
2,3 22
2,0 27
1,3 71
1,2 64
702
H6
H5
H4
H3
H2
H1
1
2
3

FIGURE 2

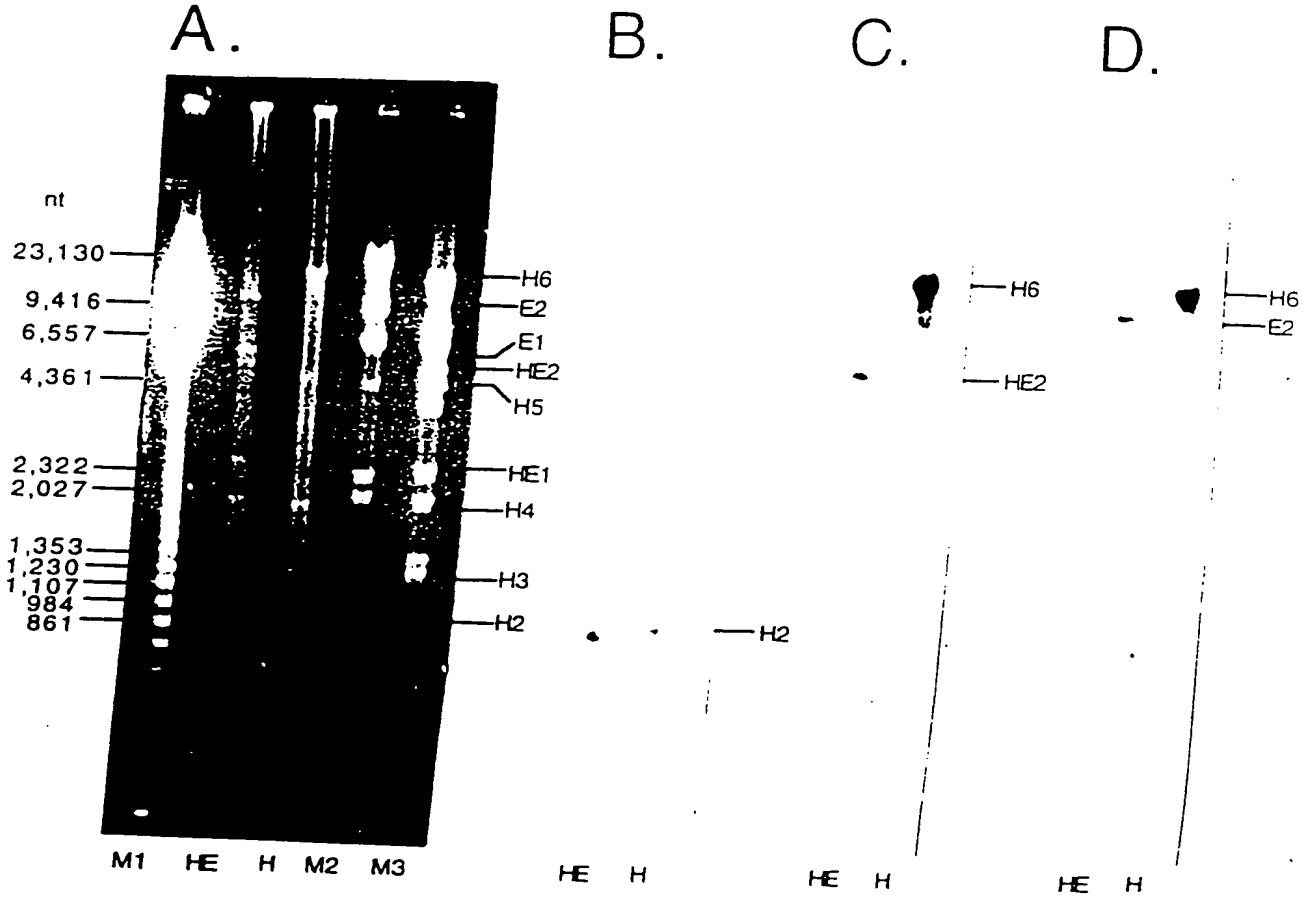
A.
B.
C.
D.
nt
23,130
9,416
6,557
4,361
2,322
2,027
1,353
1,230
1,107
984
861
H6
E2
E1
HE2
H5
HE1
H4
H3
H2
M1
HE
H
M2
M3
H6
HE2
H6
E2

FIGURE 3

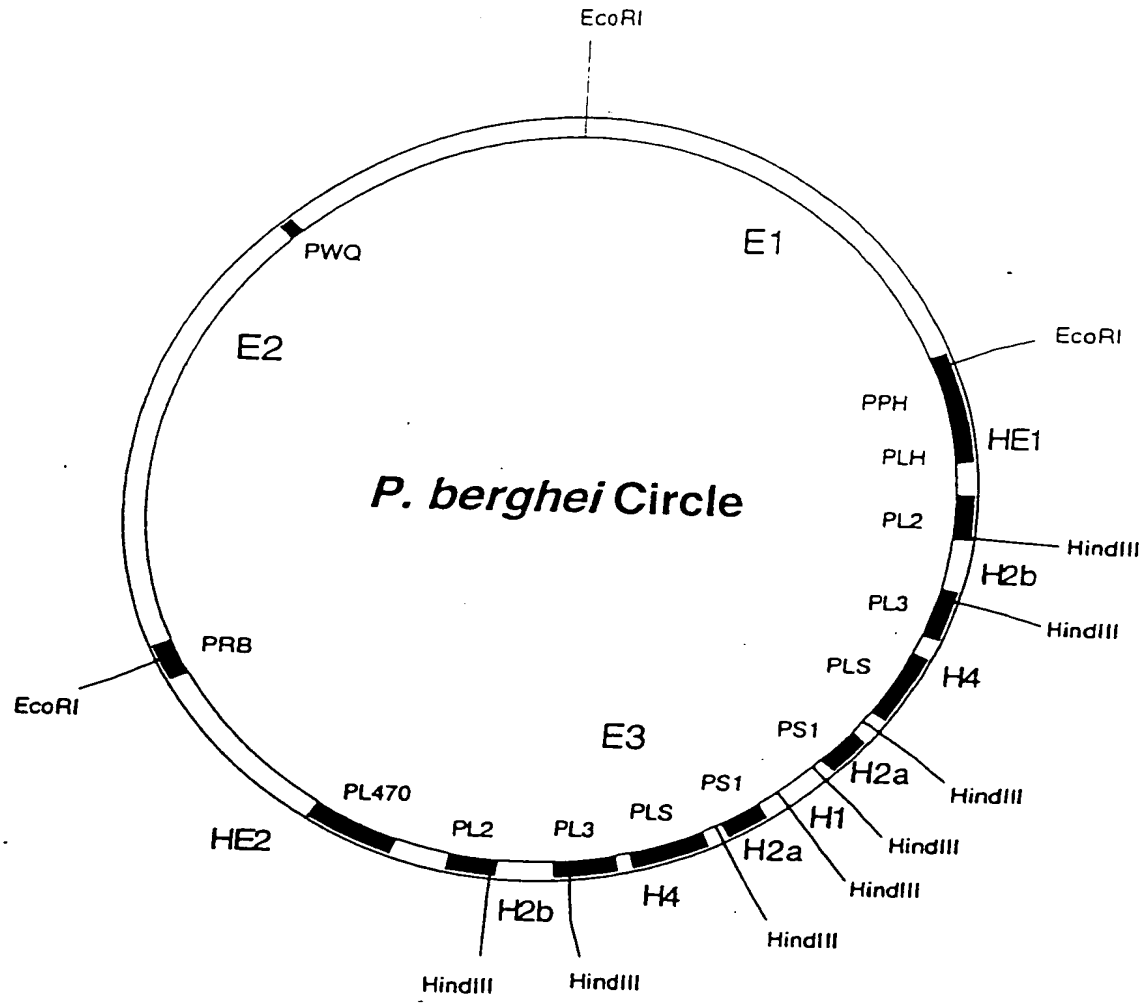
EcoRI
E1
PWQ
E2
EcoRI
PPH
HE1
PLH
P. berghei Circle
PL2
HindIII
H2b
PL3
HindIII
PRB
PLS
H4
EcoRI
E3
PS1
H2a
HindIII
PS1
PL470
PLS
H1
HindIII
HE2
PL2
PL3
H2a
HindIII
H4
H2b
HindIII
HindIII
HindIII

FIGURE 4A

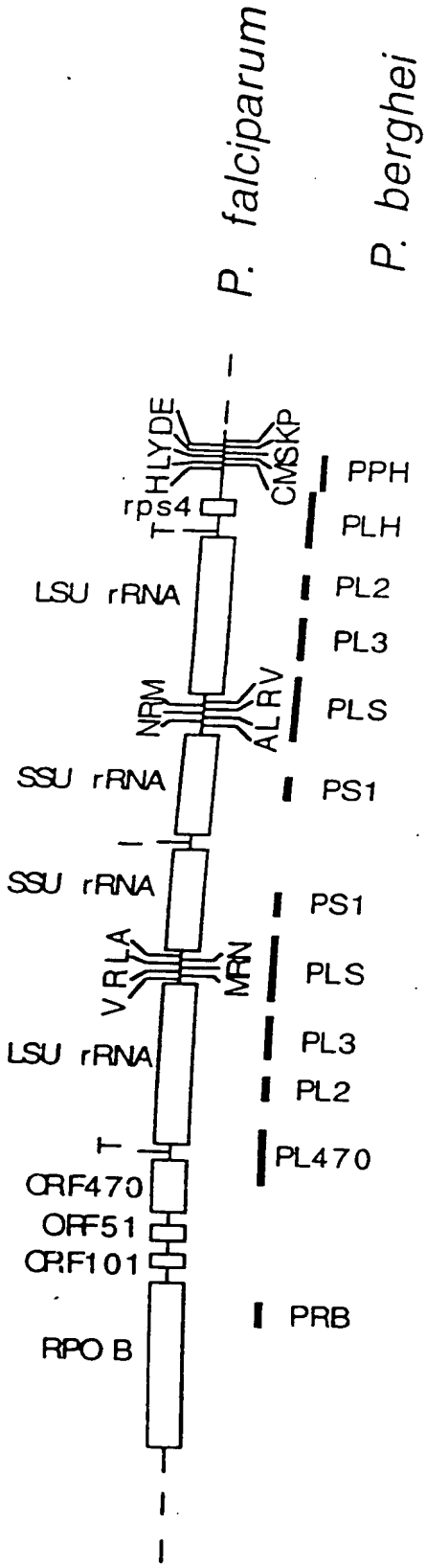
P. falciparum
P. berghei
HLYDE
CMSKP
PPH
rps4
T
PLH
LSU rRNA
PL2
PL3
NRM
ALRV
PLS
SSU rRNA
PS1
SSU rRNA
PS1
VRLA
MRN
PLS
LSU rRNA
PL3
PL2
T
PL470
ORF470
ORF51
ORF101
PRB
RPO B

FIGURE 4B

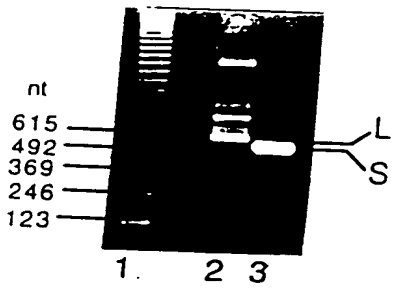

FIGURE 5

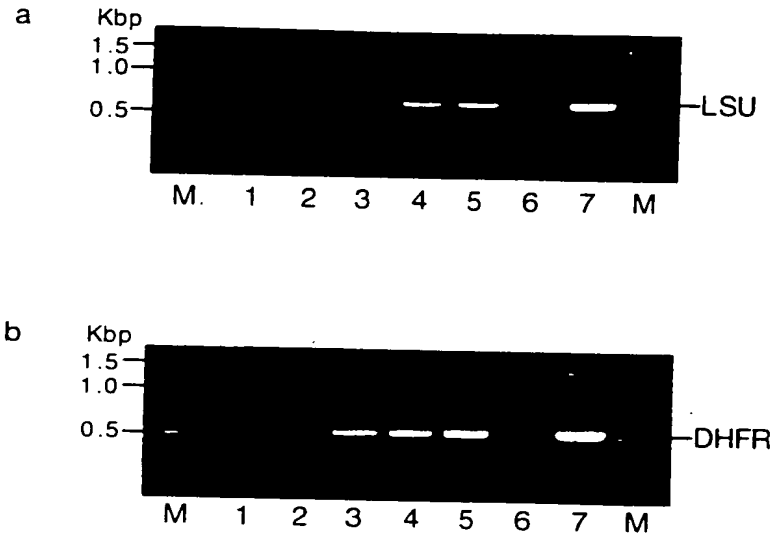

FIGURE 6

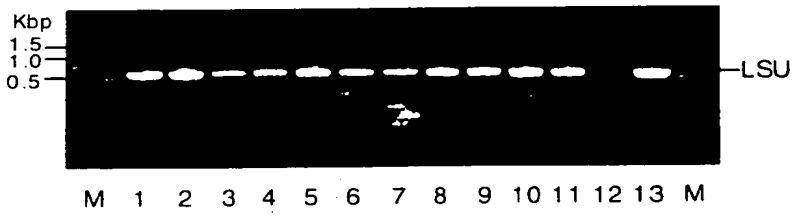

FIGURE 7

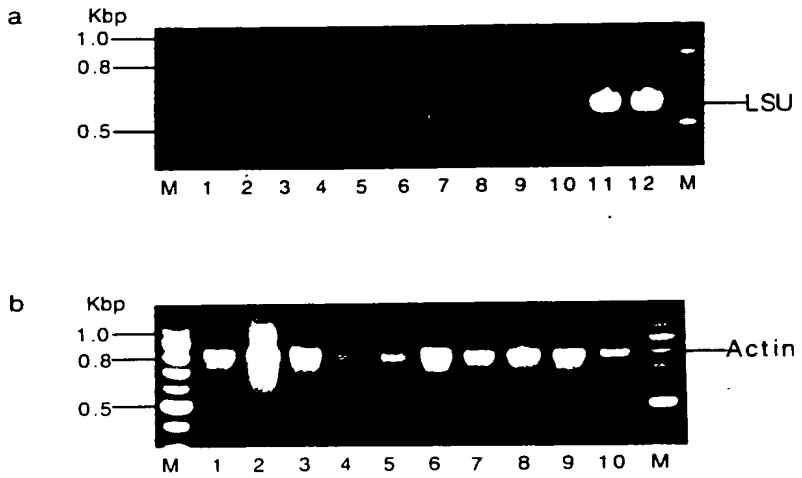
a
Kbp
1.0
0.8
0.5
LSU
M 1 2 3 4 5 6 7 8 9 10 11 12 M
b
Kbp
1.0
0.8
0.5
Actin
M 1 2 3 4 5 6 7 8 9 10 M

FIGURE 8

FIGURE 9A

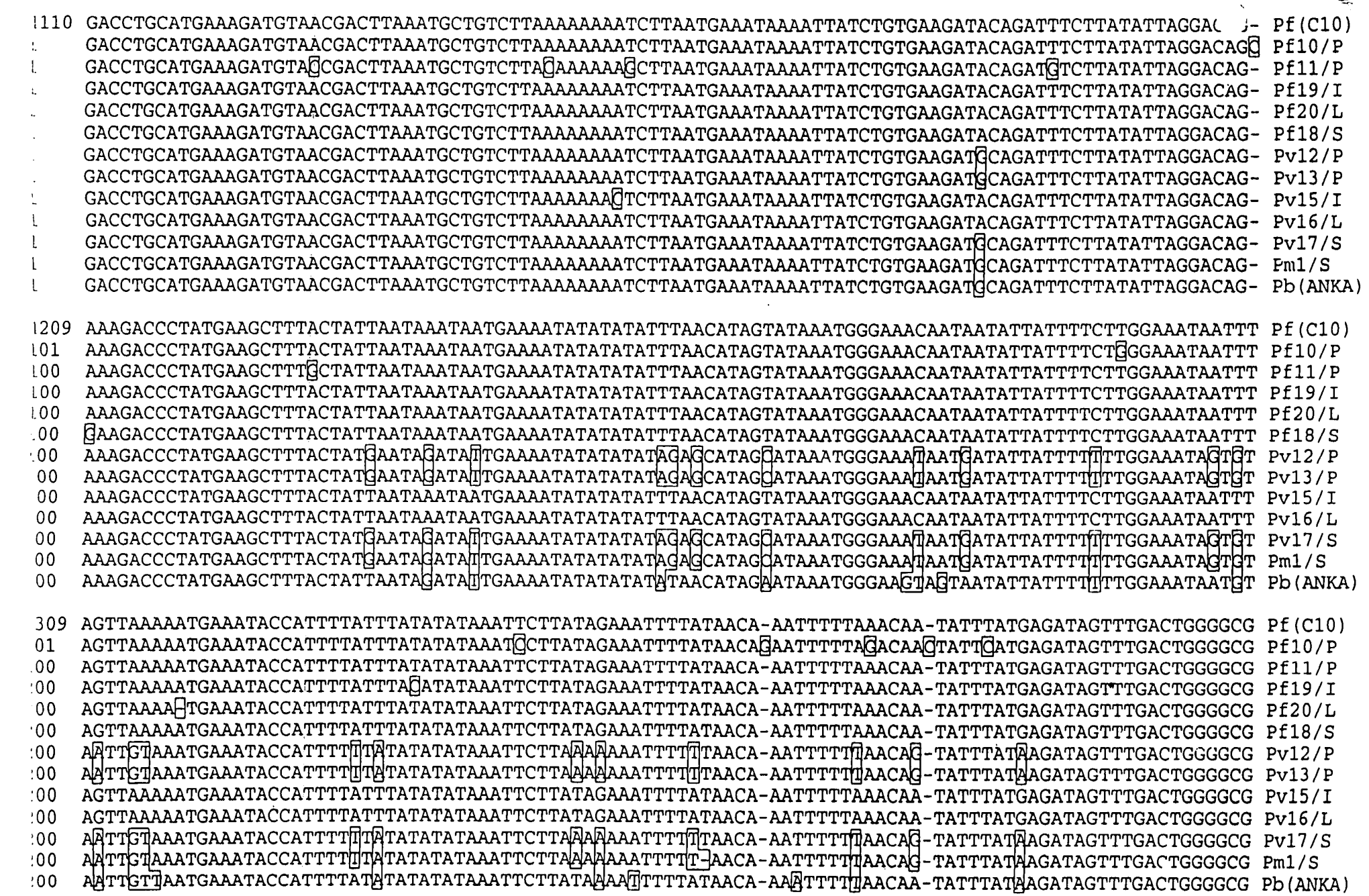
1110 GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGAC - Pf(C10)
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAGG Pf10/P
GACCTGCATGAAAGATGTAGCGACTTAAATGCTGTCTTAGAAAAAAGCTTAATGAAATAAAATTATCTGTGAAGATACAGATGTCTTATATTAGGACAG- Pf11/P
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAG- Pf19/I
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAG- Pf20/L
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAG- Pf18/S
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATGCAGATTTCTTATATTAGGACAG- Pv12/P
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATGCAGATTTCTTATATTAGGACAG- Pv13/P
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAGTCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAG- Pv15/I
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATACAGATTTCTTATATTAGGACAG- Pv16/L
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATGCAGATTTCTTATATTAGGACAG- Pv17/S
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATGCAGATTTCTTATATTAGGACAG- Pm1/S
GACCTGCATGAAAGATGTAACGACTTAAATGCTGTCTTAAAAAAAAATCTTAATGAAATAAAATTATCTGTGAAGATGCAGATTTCTTATATTAGGACAG- Pb(ANKA)
1209 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pf(C10)
101 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTGGGAAATAATTT Pf10/P
100 AAAGACCCTATGAAGCTTTGCTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pf11/P
100 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pf19/I
100 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pf20/L
100 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pf18/S
100 AAAGACCCTATGAAGCTTTACTATGAATAGATATTGAAAATATATATATAGAGCATAGCATAAATGGGAAATAATGATATTATTTTTTTGGAAATAGTGT Pv12/P
00 AAAGACCCTATGAAGCTTTACTATGAATAGATATTGAAAATATATATATAGAGCATAGCATAAATGGGAAATAATGATATTATTTTTTTGGAAATAGTGT Pv13/P
00 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pv15/I
00 AAAGACCCTATGAAGCTTTACTATTAATAAATAATGAAAATATATATATTTAACATAGTATAAATGGGAAACAATAATATTATTTTCTTGGAAATAATTT Pv16/L
00 AAAGACCCTATGAAGCTTTACTATGAATAGATATTGAAAATATATATATAGAGCATAGCATAAATGGGAAATAATGATATTATTTTTTTGGAAATAGTGT Pv17/S
00 AAAGACCCTATGAAGCTTTACTATGAATAGATATTGAAAATATATATATAGAGCATAGCATAAATGGGAAATAATGATATTATTTTTTTGGAAATAGTGT Pm1/S
00 AAAGACCCTATGAAGCTTTACTATTAATAGATATTGAAAATATATATATATAACATAGAATAAATGGGAAGTAGTAATATTATTTTTTTGGAAATAATGT Pb(ANKA)
309 AGTTAAAAATGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pf(C10)
01 AGTTAAAAATGAAATACCATTTTATTTATATATAAATGCTTATAGAAATTTTATAACAGAATTTTTAGACAAGTATTCATGAGATAGTTTGACTGGGGCG Pf10/P
00 AGTTAAAAATGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pf11/P
00 AGTTAAAAATGAAATACCATTTTATTTATGATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pf19/I
00 AGTTAAAA-TGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pf20/L
00 AGTTAAAAATGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pf18/S
00 AATTGTAAATGAAATACCATTTTTTATATATATAAATTCTTAAAAAAAATTTTTTAACA-AATTTTTTAACAG-TATTTATAAGATAGTTTGACTGGGGCG Pv12/P
00 AATTGTAAATGAAATACCATTTTTTATATATATAAATTCTTAAAAAAAATTTTTTAACA-AATTTTTTAACAG-TATTTATAAGATAGTTTGACTGGGGCG Pv13/P
00 AGTTAAAAATGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pv15/I
00 AGTTAAAAATGAAATACCATTTTATTTATATATAAATTCTTATAGAAATTTTATAACA-AATTTTTAAACAA-TATTTATGAGATAGTTTGACTGGGGCG Pv16/L
00 AATTGTAAATGAAATACCATTTTTTATATATATAAATTCTTAAAAAAAATTTTTTAACA-AATTTTTTAACAG-TATTTATAAGATAGTTTGACTGGGGCG Pv17/S
00 AATTGTAAATGAAATACCATTTTTTATATATATAAATTCTTAAAAAAAATTTTT-AACA-AATTTTTTAACAG-TATTTATAAGATAGTTTGACTGGGGCG Pm1/S
00 AATTGTTAATGAAATACCATTTTATATATATATAAATTCTTATAAAAATTTTTATAACA-AAATTTTTAACAA-TATTTATAAGATAGTTTGACTGGGGCG Pb(ANKA)

FIGURE 9B

```
4407 GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGA  TAA Pf(C10
301  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pf10/P
298  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pf11/P
298  GTCTCCTCCTATATATAAACAGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pf19/I
297  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pf20/L
298  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pf18/S
298  GTCTCCTCCTATATAAAAACGGAGGAGTACAAAGTTATATATGTTATATAAAGATATA-TATATAATTAACTGTAAAATTAACAAATTAAACAGAGATTA Pv12/P
298  GTCTCCTCCTATATAAAAACGGAGGAGTACAAAGTTATATATGTTATATAAAGATATA-TATATAATTAACTGTAAAATTGACAAATTAAACAGAGATTA Pv13/P
298  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pv15/I
298  GTCTCCTCCTATATATAAACGGAGGAGTACAATGTTATATTTATTATATAAAGATATAATATATAATTAACTGTAAAATTTACAAATTAAACAGAGATAA Pv16/L
298  GTCTCCTCCTATATAAAAACGGAGGAGTACAAAGTTATATATGTTATATAAAGATATA-TATATAATTAACTGTAAAATTAACAAATTAAACAGAGATTA Pv17/S
297  GTCTCCTCCTATATAAAAACGGAGGAGTACAAAGTTATATATGTTATATAAAGATATA-TATATAATTAACTGTAAAATTAACAAATTAAACAGAGATTA Pm1/S
298  GTCTCCTCCTATATAAAAACGGAGGTGTACAATGTTATATTTATTATATAAAGATAAA-TATATAATTAACTGTAAAATTTACAAATTAAACAGAGATTA Pb(ANKA

4507 ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf(C10
401  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf10/P
398  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf11/P
398  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf19/I
397  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf20/L
398  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pf18/S
397  ATGTCGGTCTTAATGATCCGATAATTATTTAATGATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pv12/P
397  ATGTCGGTCTTAATGATCCGATAATTATTTAATGATAAAATTATCGCTTAACGGATAAAAGTTACTGTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pv13/P
398  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pv15/I
398  ATGTCGGTCTTAATGATCCGATAATTATTTAGTAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pv16/L
397  ATGTCGGTCTTAATGATCCGATAATTATTTAATGATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pv17/S
396  ATGTCGGTCTTAATGATCCGATAATTATTTAATGATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pm1/S
397  ATGTCGGTCTTAATGATCCGATAATTATTTAATAATAAAATTATCGCTTAACGGATAAAAGTTACTCTAGGGATAACAGGCTAATCTTTTCCGAGAGTCC Pb(ANKA

4607 ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf(C10)
501  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf10/P
498  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGCCCCAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf11/P
498  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf19/I
497  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf20/L
498  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pf18/S
497  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pv12/P
497  ATATTGACGAAAAGGTTCGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pv13/P
498  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTTACGCCTATTAAAGCGATAC  Pv15/I
498  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTTCGCCTATTAAAGCGATAC  Pv16/L
497  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pv17/S
496  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pm1/S
497  ATATTGACGAAAAGGTTTGGCACCTCGATGTCGGCTTATCGCATCCTAAGCAGTAGTATGTTTTAAGGGTAAGTCTGTT-CGCCTATTAAAGCGATAC  Pb(ANKA
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